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(21) International Application Number: PCT/US99/11942 (22) International Filing Date: 28 May 1999 (28.05.99) (30) Priority Data: 60/087,306 29 May 1998 (29.05.98) US (71) Applicant: HESKA CORPORATION [US/US]; 1613 Prospect Parkway, Fort Collins, CO 80525 (US). (72) Inventors: SIM, Gek-Kee; 3622 Terry Point Drive, Fort Collins, CO 80524 (US). YANG, Shumin; 2624 Shavano Court, Fort Collins, CO 80525 (US). DREITZ, Matthew, J.; 4324 Winterstone, Fort Collins, CO 80525 (US). WONDERLING, Ramani, S.; 5808 Park Ridge Court, Fort Collins, CO 80528 (US). (74) Agents: HANLEY, Elizabeth, A. et al.; Lahive & Cockfield, LLP, 28 State Street, Boston, MA 02109 (US).	(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>	
(54) Title: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF (57) Abstract The present invention relates to canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, and/or feline GM-CSF proteins; to canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, and/or feline GM-CSF nucleic acid molecules, including those that encode canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, and/or feline GM-CSF proteins, respectively; to antibodies raised against such proteins; and to inhibitory compounds that regulate such proteins. The present invention also includes methods to identify and obtain such proteins, nucleic acid molecules, antibodies, and inhibitory compounds. Also included in the present invention are therapeutic compositions comprising such proteins, nucleic acid molecules, antibodies and/or inhibitory compounds as well as the use of such therapeutic compositions to regulate an immune response in an animal.		

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CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF

FIELD OF THE INVENTION

The present invention relates to canine interleukin-4, canine or feline Flt-3
5 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine
interleukin-13, feline interferon alpha, or feline GM-CSF nucleic acid molecules,
proteins encoded by such nucleic acid molecules, antibodies raised against such proteins
and/or inhibitors of such proteins or nucleic acid molecules. The present invention also
includes therapeutic compositions comprising such nucleic acid molecules, proteins,
10 antibodies and/or inhibitors, as well as their use to regulate an immune response in an
animal.

BACKGROUND OF THE INVENTION

Regulating immune responses in animals is important in disease management.
Immune responses can be regulated by modifying the activity of immunoregulatory
15 molecules and immune cells.

Several immunoregulatory molecules have been found in humans and other
mammal species. Interleukin-4, produced by activated type 2 helper cells (T_H2 cells),
has a number of functions. These functions include promotion of naive T cells and B
cells to differentiate and proliferate. IL-4 promotes T_H2 differentiation and inhibits T_H1
20 development. FMS-like tyrosine kinase 3, (Flt-3 ligand) stimulates the expansion and
mobilization of hematopoietic precursor cell stimulating activity. CD40 is a type I
transmembrane protein expressed on antigen presenting cells, such as B lymphocytes,
and other types of cells such as endothelial cells, epithelial cells, and fibroblasts. CD40
ligand (also known as CD154) is a type II transmembrane protein that is preferentially
25 expressed on activated T lymphocytes. The CD40-CD154 interaction regulates diverse
pathways of the immune system, including B cell proliferation, immunoglobulin
production and class switching by B cells, activation and clonal expansion of T cells,
activity of antigen presenting cells, growth and differentiation of epithelial cells, and
regulation of inflammatory responses at mucosal and cutaneous sites. Interleukin-5 is
30 produced by activated type 2 helper cells (T_H2), mast cells, and eosinophils. Its main

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functions include promotion of growth and differentiation of eosinophils and generation of cytotoxic T cells from thymocytes. Interleukin-13 is produced by T_H1 and T_H2 cells, and promotes growth and differentiation of B cells, up-regulation of MHC class II and CD23 expression on monocytes/macrophages and B cells; and inhibition of production
5 of inflammatory cytokines such as IL-1 α , IL-1 β , IL-6, IL-8, IL-10, IL-12, among others. Interferon alpha is an antiviral protein that has three major functions: it inhibits viral replication by activating cellular genes that destroy mRNA and inhibit protein translation, it induces MHC class I expression in non virally-infected cells, increasing resistance to NK cells, and can activate NK cells. GM-CSF, (granulocyte-macrophage
10 colony-stimulating factor) stimulates the production of granulocytes and macrophages.

Prior investigators have disclosed sequences encoding feline IL-4 (Lerner et al., Genbank Accession No. U39634); porcine IL-4 (Zhou et al., Genbank Accession No. L12991); bovine IL-4 (Heussler, V.T., et al., *Gene*, vol. 114, pp. 273-278, 1992); ovine IL-4 (Seow, H.-F., et al., *Gene*, vol. 124, pp. 291-293, 1993); human IL-4 (Yokota, T., et
15 al., *Proc. Natl. Acad. Sci. U.S.A.*, vol. 83(16), pp. 5894-5898, 1986); and murine IL-4 (Sideras, P., et al., *Adv. Exp. Med. Biol.*, vol. 213, pp. 227-236, 1987). Prior investigators have disclosed sequences encoding murine Flt-3 ligand (McClanahan et al., Genbank Accession No. U44024); and human Flt-3 ligand (Lyman et al., *Blood*, vol. 83, pp. 2795-2801, 1994). Prior investigators have disclosed sequences encoding human
20 CD40 (Stamenkovic et al., *EMBO J.*, vol. 8:1403-1410, 1989, GenBank Accession No. (X60592), bovine CD40 (Hirano et al., *Immunology*, vol. 90, pp. 294-300, 1997, GenBank Accession No. U57745), and murine CD40 (Grimaldi et al., *J. Immunol.*, vol. 143, pp.3921-3926, 1992; Torres and Clark, *J. Immunol.*, vol. 148, pp. 620-626, 1992, GenBank Accession No. M83312). Prior investigators have disclosed sequences
25 encoding human CD154 (Graf et al., *Eur. J. Immunol.*, vol. 22, pp. 3191-3194, 1992; Hollenbaugh, et al., *EMBO J.*, vol. 11:4313-4321, 1992; Gauchat et al., *FEBS lett.*, vol. 315, pp. 259-266, 1993; GenBank Accession Nos L07414, X68550, Z15017, X67878, respectively); bovine CD154 (Mertens et al., *Immunogenetics*, vol. 42, pp. 430-431, GenBank Accession No. Z48468); and murine CD154 (Armitage et al., *Nature*, vol. 357,
30 pp. 80-82; 1992, GenBank Accession No. X65453). Prior investigators have disclosed sequences encoding feline interleukin-5 (Padrid et al., *Am. J. Vet. Res.*, vol. 59, pp.

1263-1269, 1998, GenBank Accession No. AF025436) and human interleukin-5 (Azuma et al., *Nucleic Acids Res.*, vol. 14, pp. 9149-9158, 1986, GenBank Accession No. X04688). Prior investigators have disclosed sequences encoding human interleukin-13 (McKenzie et al., *Proc. Natl Acad. Sci. USA*, vol. 90, pp. 3735-3739, 1993; Minty et al.,
5 *Nature*, vol. 362, pp. 248-250, 1993, GenBank Accession Nos L06801 and X69079, respectively); murine interleukin-13 (Brown et al., *J. Immunol.*, vol. 142, pp. 679-687, 1989, GenBank Accession No M23504); and rat interleukin-13 (Lakkis et al., *Biochem. Biophys. Res. Commun.*, Vol. 197, pp. 612-618, 1993, GenBank Accession No. L26913). Prior investigators have disclosed sequences encoding feline interferon (Nakamura, N.,
10 Sudo, T., Matsuda, S., Yanai, A., *Biosci. Biotechnol. Biochem.* (1992)Vol: 56 pp 211-214, GenBank accession # E02521). Prior investigators have also disclosed sequences encoding feline GM-CSF (direct submission to GenBank, Accession No. AF053007)

There remains a need for compounds and methods to regulate an immune
15 response by manipulation of the function of canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF.

SUMMARY OF THE INVENTION

The present invention relates to canine interleukin-4, canine or feline Flt-3
20 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF nucleic acid molecules, proteins encoded by such nucleic acid molecules, antibodies raised against such proteins and/or inhibitors of such proteins or nucleic acid molecules. Identification of the nucleic acid molecules of the present invention is unexpected because initial attempts to obtain
25 nucleic acid molecules using PCR were unsuccessful. After numerous attempts, the inventors discovered specific primers that were useful for isolating such nucleic acid molecules.

One embodiment of the present invention is an isolated nucleic acid molecule selected from the group consisting of: (a) an isolated nucleic acid molecule comprising a
30 nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:19, and/or SEQ ID NO:21 or a

homolog thereof, wherein said homolog has an at least about 50 contiguous nucleotide region identical in sequence to a 50 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:19, and/or SEQ ID NO:21; (b) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:36, and/or SEQ ID NO:37 or a homolog thereof, wherein said homolog has an at least 40 contiguous nucleotide region identical in sequence to a 40 contiguous nucleotide region of a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:36, and/or SEQ ID NO:37; (c) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, and/or SEQ ID NO:50, and/or a homolog thereof, wherein said homolog has an at least 30 contiguous nucleotide region identical in sequence to a 30 contiguous nucleotide region of a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, and/or SEQ ID NO:50; (d) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, and/or SEQ ID NO:59, and/or a homolog thereof, wherein said homolog has an at least 40 contiguous nucleotide region identical in sequence to a 40 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, and/or SEQ ID NO:59; (e) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:60 and/or SEQ ID NO:62, and/or a homolog thereof, wherein said homolog has an at least 30

contiguous nucleotide region identical in sequence to a 30 contiguous nucleotide region of a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:60 and/or SEQ ID NO:62; (f) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69 and/or SEQ ID NO:71, and/or a homolog thereof, wherein said homolog has an at least 45 contiguous nucleotide region identical in sequence to a 45 nucleotide region of a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69 and/or SEQ ID NO:71; (g) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, and/or SEQ ID NO:79, and/or a homolog thereof, wherein said homolog has an at least 35 contiguous nucleotide region identical in sequence to a 35 contiguous nucleotide region of a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, and/or SEQ ID NO:79; (h) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, and/or SEQ ID NO:87, and/or a homolog thereof, wherein said homolog has an at least 45 contiguous nucleotide region identical in sequence to a 45 contiguous nucleotide region of a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, and/or SEQ ID NO:87; (i) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, and/or SEQ ID NO:106, and/or a homolog thereof, wherein said homolog has an at least 15 contiguous nucleotide region identical to a 15 contiguous nucleotide region of a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID

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NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, and/or SEQ ID NO:106; (j) an isolated nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:118; and/or (k) an isolated nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:126.

Another embodiment of the present invention is an isolated nucleic acid molecule selected from the group consisting of: (a) a nucleic acid molecule having a nucleic acid sequence that is at least about 92 percent identical to a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:19, and/or SEQ ID NO:21; (b) a nucleic acid molecule having a nucleic acid sequence that is at least about 75 percent identical to a nucleic acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:36, and/or SEQ ID NO:37; (c) a nucleic acid molecule having a nucleic acid sequence that is at least about 75 percent identical to a nucleic acid sequence selected from the group consisting of SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, and/or SEQ ID NO:50; (d) a nucleic acid molecule having a nucleic acid sequence that is at least about 70 percent identical to a nucleic acid sequence selected from the group consisting of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, and/or SEQ ID NO:59; (e) a nucleic acid molecule having a nucleic acid sequence that is at least about 70 percent identical to a nucleic acid sequence selected from the group consisting of SEQ ID NO:60 and/or SEQ ID NO:62; (f) a nucleic acid molecule having a nucleic acid sequence that is at least about 85 percent identical to a nucleic acid sequence selected from the group consisting of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, and/or SEQ ID NO:71; (g) a nucleic acid molecule having a nucleic acid

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sequence that is at least about 91 percent identical to a nucleic acid sequence selected from the group consisting of SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, and/or SEQ ID NO:79; (h) a nucleic acid molecule having a nucleic acid sequence that is at least about 90 percent identical to a nucleic acid

5 sequence selected from the group consisting of SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, and/or SEQ ID NO:87; (i) a nucleic acid molecule having a nucleic acid sequence that is at least about 65 percent identical to a nucleic acid sequence selected from the group consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:94, SEQ ID

10 NO:95, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, and/or SEQ ID NO:106; (j) a nucleic acid molecule having a nucleic acid sequence that is selected from the group consisting of SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:116, and/or SEQ ID NO:118; and/or (k) a nucleic acid

15 molecule having a nucleic acid sequence that is selected from the group consisting of SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, and/or SEQ ID NO:126.

Yet another embodiment of the present invention is an isolated nucleic acid molecule selected from the group consisting of: (a) a nucleic acid molecule having a

20 nucleic acid sequence encoding an IL-4 protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 85 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:2 and/or SEQ ID NO:20 and/or (ii) a protein comprising a fragment of at least 20 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:2 and/or SEQ ID

25 NO:20; (b) a nucleic acid molecule having a nucleic acid sequence encoding a Flt-3 ligand protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 75 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, and/or SEQ ID NO:34 and/or (ii) a protein comprising a fragment of at least 25

30 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, and/or SEQ ID NO:34; (c) a

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- nucleic acid molecule having a nucleic acid sequence encoding a Flt-3 ligand protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 75 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:44 and/or SEQ ID NO:49 and/or (ii) a protein comprising a
- 5 fragment of at least 25 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:44 and/or SEQ ID NO:49;
- (d) a nucleic acid molecule having a nucleic acid sequence encoding a CD40 protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 70 percent identical to an amino acid sequence selected from the group
- 10 consisting of SEQ ID NO:53 and/or SEQ ID NO:58 and/or (ii) a protein comprising a fragment of at least 30 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:53 and/or SEQ ID NO:58; (e) a nucleic acid molecule having a nucleic acid sequence encoding a CD40 protein selected from the group consisting of
- (i) a protein having an amino acid sequence that is at least about 60 percent identical to
- 15 an amino acid sequence comprising SEQ ID NO:61 and/or (ii) a protein comprising a fragment of at least 20 amino acids of an amino acid sequence comprising SEQ ID NO:61; (f) a nucleic acid molecule having a nucleic acid sequence encoding a CD154 protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 80 percent identical to an amino acid sequence selected from the
- 20 group consisting of SEQ ID NO:65 and/or SEQ ID NO:70, and/or (ii) a protein comprising a fragment of at least 35 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:65 and/or SEQ ID NO:70; (g) a nucleic acid molecule having a nucleic acid sequence encoding a CD154 protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 85
- 25 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:73 and/or SEQ ID NO:78, and/or (ii) a protein comprising a fragment of at least 50 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:73 and/or SEQ ID NO:78; (h) a nucleic acid molecule having a nucleic acid sequence encoding an IL-5 protein selected from the group consisting of (i) a protein
- 30 having an amino acid sequence that is at least about 85 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:81 and/or SEQ ID

NO:86 and/or (ii) a protein comprising a fragment of at least 20 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:81 and/or SEQ ID NO:86; (i) a nucleic acid molecule having a nucleic acid sequence encoding an IL-13 protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 70 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, and/or SEQ ID NO:105 and/or (ii) a protein comprising a fragment of at least 15 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, and/or SEQ ID NO:105; (j) a nucleic acid molecule having a nucleic acid sequence encoding an interferon alpha protein having an amino acid sequence that is selected from the group consisting of amino acid sequence SEQ ID NO:108, SEQ ID NO:111, SEQ ID NO:114, and/or SEQ ID NO:117; (k) a nucleic acid molecule having a nucleic acid sequence encoding a GMCSF protein having an amino acid sequence that is selected from the group consisting of amino acid sequence SEQ ID NO:120, SEQ ID NO:125, and/or (l) a nucleic acid molecule comprising a complement of any of said nucleic acid molecules as set forth in (a), (b), (c), (d), (e), (f), (g), (h), (i), (j), and/or (k), wherein said IL-4 protein elicits an immune response against an IL-4 protein selected from the group consisting of SEQ ID NO:2 and/or SEQ ID NO:20 and/or is a protein with interleukin-4 activity, said Flt-3 ligand protein elicits an immune response against a Flt-3 ligand protein selected from the group consisting of SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, SEQ ID NO:34, SEQ ID NO:44, and/or SEQ ID NO:49 and/or is a protein with Flt-3 ligand activity, said CD40 protein elicits an immune response against a CD40 protein selected from the group consisting of SEQ ID NO:53, SEQ ID NO:58, and/or SEQ ID NO:61 and/or is a protein with CD40 activity, said CD154 protein elicits an immune response against a CD154 protein selected from the group consisting of SEQ ID NO:65, SEQ ID NO:70, SEQ ID NO:73, and/or SEQ ID NO:78 and/or is a protein with CD154 activity, said IL-5 protein elicits an immune response against a IL-5 protein selected from the group consisting of SEQ ID NO:81 and/or SEQ ID NO:86 and/or is a protein with IL-5 activity, said IL-13 protein elicits an immune response against an IL-13 protein selected from the group consisting of SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, and/or SEQ ID NO:105

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and/or is a protein with IL-13 activity, said interferon alpha protein elicits an immune response against an interferon alpha protein selected from the group consisting of SEQ ID NO:108, SEQ ID NO:111, SEQ ID NO:114, and/or SEQ ID NO:117 and/or is a protein with interferon alpha activity, and/or said GMCSF protein elicits an immune response against a GMCSF protein selected from the group consisting of SEQ ID NO:120 and/or SEQ ID NO:125 and/or is a protein with GM-CSF activity.

The present invention also includes methods to produce any of the proteins of the present invention using nucleic acid molecules of the present invention and recombinantly using such nucleic acid molecules.

10 The present invention also includes an isolated protein selected from the group consisting of: (a) (i) an isolated protein of at least about 20 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 60 contiguous nucleotide region identical in sequence to a 60 contiguous nucleotide region of a nucleic acid sequence selected from the group
15 consisting of SEQ ID NO:1, SEQ ID NO:4, and/or SEQ ID NO:19; and/or (ii) an isolated protein of at least about 20 amino acids in length, wherein said protein has an at least 20 contiguous amino acid region identical in sequence to a 20 contiguous amino acid region selected from the group consisting of SEQ ID NO:2 and/or SEQ ID NO:20, wherein said isolated protein elicits an immune response against a canine IL-4 protein
20 and/or has IL-4 activity; (b) (i) an isolated protein of at least about 20 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 60 contiguous nucleotide region identical in sequence to a 60 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:9, SEQ ID NO:22, SEQ ID NO:25, SEQ ID
25 NO:28, SEQ ID NO:30, SEQ ID NO:33, and/or SEQ ID NO:36; and/or (ii) an isolated protein of at least about 20 amino acids in length, wherein said protein has an at least 20 contiguous amino acid region identical in sequence to a 20 contiguous amino acid region selected from the group consisting of SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, and/or SEQ ID NO:34, wherein said isolated protein is capable of
30 eliciting an immune response against a canine Flt-3 ligand protein and/or has Flt-3 activity; (c) (i) an isolated protein of at least about 20 amino acids in length, wherein

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said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 60 contiguous nucleotide region identical in sequence to a 60 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:46, and/or SEQ ID NO:48;

5 and/or (ii) an isolated protein of at least about 20 amino acids in length, wherein said protein has an at least 20 contiguous amino acid region identical in sequence to a 20 contiguous amino acid region selected from the group consisting of SEQ ID NO:44 and/or SEQ ID NO:49, wherein said isolated protein is capable of eliciting an immune response against a feline Flt-3 ligand protein and/or has Flt-3 activity; (d)(i) an isolated

10 protein of at least about 30 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 90 contiguous nucleotide region identical in sequence to a 90 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:55, and/or SEQ ID NO:57; and/or (ii) an isolated protein of at least about

15 30 amino acids in length, wherein said protein has an at least 30 contiguous amino acid region identical in sequence to a 30 contiguous amino acid region selected from the group consisting of SEQ ID NO:53, SEQ ID NO:58, wherein said isolated protein is capable of eliciting an immune response against a canine CD40 protein and/or has CD40 activity; (e) (i) an isolated protein of at least about 20 amino acids in length, wherein

20 said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 60 contiguous nucleotide region identical in sequence to a 60 contiguous nucleotide region of a nucleic acid sequence comprising Seq id no:60; and/or (ii) an isolated protein of at least about 20 amino acids in length, wherein said protein has an at least 20 contiguous amino acid region identical in sequence to a 20 contiguous amino

25 acid region comprising the amino acid sequence SEQ ID NO:61, wherein said isolated protein is capable of eliciting an immune response against a feline CD40 protein and/or has CD40 activity; (f)(i) an isolated protein of at least about 35 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 105 contiguous nucleotide region identical in sequence to a 105

30 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:67, and/or SEQ ID NO:69;

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and/or (ii) an isolated protein of at least about 35 amino acids in length, wherein said protein has an at least 35 contiguous amino acid region identical in sequence to a 35 contiguous amino acid region selected from the group consisting of SEQ ID NO:65 and/or SEQ ID NO:70, wherein said isolated protein is capable of eliciting an immune response against a canine CD154 protein and/or has CD154 activity; (g)(i) an isolated protein of at least about 50 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 150 contiguous nucleotide region identical in sequence to a 150 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:72, SEQ ID NO:75, and/or SEQ ID NO:77; and/or (ii) an isolated protein of at least about 50 amino acids in length, wherein said protein has an at least 50 contiguous amino acid region identical in sequence to a 50 contiguous amino acid region selected from the group consisting of SEQ ID NO:73 and/or SEQ ID NO:78, wherein said isolated protein is capable of eliciting an immune response against a feline CD154 protein and/or has CD154 activity; (h)(i) an isolated protein of at least about 20 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 60 contiguous nucleotide region identical in sequence to a 60 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:80, SEQ ID NO:83, and/or SEQ ID NO:85; and/or (ii) an isolated protein of at least about 20 amino acids in length, wherein said protein has an at least 20 contiguous amino acid region identical in sequence to a 20 contiguous amino acid region selected from the group consisting of SEQ ID NO:81 and/or SEQ ID NO:86, wherein said isolated protein is capable of eliciting an immune response against a canine IL-5 protein and/or has IL-5 activity; (i)(i) an isolated protein of at least about 15 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 45 contiguous nucleotide region identical in sequence to a 45 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:102, and/or SEQ ID NO:104; and/or (ii) an isolated protein of at least about 15 amino acids in length, wherein said protein has an at least 15 contiguous amino acid region identical in

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sequence to a 15 contiguous amino acid region selected from the group consisting of SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, and/or SEQ ID NO:105, wherein said isolated protein is capable of eliciting an immune response against a canine IL-13 protein and/or has IL-13 activity; (j) (i) an isolated protein encoded by a nucleic acid molecule selected from the group consisting of SEQ ID NO:107, SEQ ID NO:110, SEQ ID NO:113, and/or SEQ ID NO:116, and/or (ii) an isolated protein selected from the group consisting of SEQ ID NO:108, SEQ ID NO:111, SEQ ID NO:114, and/or SEQ ID NO:117, wherein said isolated protein is capable of eliciting an immune response against a feline interferon alpha protein and/or has interferon alpha activity; (k) (i) an isolated protein encoded by a nucleic acid molecule selected from the group consisting of SEQ ID NO:119, SEQ ID NO:122, and/or SEQ ID NO:124, and/or (ii) an isolated protein selected from the group consisting of SEQ ID NO:120 and/or SEQ ID NO:125, wherein said isolated protein is capable of eliciting an immune response against a feline GM-CSF and/or has GM-CSF activity.

15 The present invention also includes an isolated protein selected from the group consisting of: (a) a protein having an amino acid sequence that is at least about 85 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:2 and/or SEQ ID NO:20; (b) a protein having an amino acid sequence that is at least about 75 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, and/or SEQ ID NO:34; (c) a protein having an amino acid sequence that is at least about 75 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:44 and/or SEQ ID NO:49; (d) a protein having an amino acid sequence that is at least about 70 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:53 and/or SEQ ID NO:58; (e) a protein having an amino acid sequence that is at least about 60 percent identical to an amino acid sequence comprising SEQ ID NO:61; (f) a protein having an amino acid sequence that is at least about 80 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:65 and/or SEQ ID NO:70; (g) a protein having an amino acid sequence that is at least about 85 percent identical to the amino acid sequence SEQ ID NO:73 and/or SEQ ID NO:78; (h) a protein having an amino acid sequence that is at least about 85 percent

identical to an amino acid sequence selected from the group consisting of SEQ ID NO:81 and/or SEQ ID NO:86; (i) a protein having an amino acid sequence that is at least about 70 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, and/or SEQ ID NO:105; (j) a
5 protein having an amino acid sequence selected from the group consisting of SEQ ID NO:108, SEQ ID NO:111, SEQ ID NO:114, and/or SEQ ID NO:117; and/or (k) a protein having an amino acid sequence selected from the group consisting of SEQ ID NO:120, and/or SEQ ID NO:125.

The present invention also includes isolated antibodies that selectively bind to a
10 protein of the present invention.

One aspect of the present invention is a therapeutic composition that, when administered to an animal, regulates an immune response in said animal, said therapeutic composition comprising a therapeutic compound selected from the group consisting of: an immunoregulatory protein of the present invention; a mimetope of any of said
15 immunoregulatory proteins; and a multimeric form of any of said immunoregulatory proteins; an isolated nucleic acid molecule of the present invention; an antibody that selectively binds to any of said immunoregulatory proteins; and/or an inhibitor of a immunoregulatory protein activity identified by its ability to inhibit the activity of any of said immunoregulatory proteins. Yet another aspect of the present invention is a
20 method to regulate an immune response in an animal comprising administering to the animal a therapeutic composition of the present invention.

The present invention also includes a method to produce an immunoregulatory protein, said method comprising culturing a cell capable of expressing said protein, said protein being encoded by a nucleic acid molecule of the present invention.

25 One embodiment of the present invention is a method to identify a compound capable of regulating an immune response in an animal, said method comprising: (a) contacting an isolated canine IL-4 protein of the present invention with a putative inhibitory compound under conditions in which, in the absence of said compound, said protein has T cell proliferation stimulating activity; and determining if said putative
30 inhibitory compound inhibits said activity; (b) contacting an isolated canine Flt-3 ligand protein of the present invention with a putative inhibitory compound under conditions in

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which, in the absence of said compound, said protein has dendritic precursor cell proliferation stimulating activity; and determining if said putative inhibitory compound inhibits said activity; (c) contacting an isolated feline Flt-3 ligand protein of the present invention with a putative inhibitory compound under conditions in which, in the absence of said compound, said protein has dendritic precursor cell proliferation stimulating activity; and determining if said putative inhibitory compound inhibits said activity; (d) contacting an isolated canine CD40 protein of the present invention with a putative inhibitory compound under conditions in which, in the absence of said compound, said protein has CD40 ligand binding activity; and determining if said putative inhibitory compound inhibits said activity; (e) contacting an isolated feline CD40 protein of the present invention with a putative inhibitory compound under conditions in which, in the absence of said compound, said protein has CD40 ligand binding activity; and determining if said putative inhibitory compound inhibits said activity; (f) contacting an isolated canine CD154 protein of the present invention with a putative inhibitory compound under conditions in which, in the absence of said compound, said protein has B cell proliferation activity; and determining if said putative inhibitory compound inhibits said activity; (g) contacting an isolated feline CD154 protein of the present invention with a putative inhibitory compound under conditions in which, in the absence of said compound, said protein has B cell proliferation activity; and determining if said putative inhibitory compound inhibits said activity; (h) contacting an isolated canine IL-5 protein of the present invention with a putative inhibitory compound under conditions in which, in the absence of said compound, said protein has TF-1 cell proliferation activity; and determining if said putative inhibitory compound inhibits said activity; (i) contacting an isolated canine IL-13 protein of the present invention with a putative inhibitory compound under conditions in which, in the absence of said compound, said protein has TF-1 cell proliferation activity; and determining if said putative inhibitory compound inhibits said activity; (j) contacting an isolated feline IFN α protein of the present invention with a putative inhibitory compound under conditions in which, in the absence of said compound, said protein has inhibition of proliferation of GM-CSF stimulated TF-1 cell activity; and determining if said putative inhibitory compound inhibits said activity; or (k) contacting an isolated feline GMCSF protein of the present

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invention with a putative inhibitory compound under conditions in which, in the absence of said compound, said protein has TF-1 cell proliferation activity; and determining if said putative inhibitory compound inhibits said activity.

DETAILED DESCRIPTION OF THE INVENTION

5 The present invention provides for isolated canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF proteins, isolated canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline
10 GM-CSF nucleic acid molecules, antibodies directed against canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF proteins, and compounds derived therefrom that regulate the immune response of an animal (e.g. inhibitors, antibodies and peptides).

15 Canine IL-4 protein can refer to a canine IL-4 protein, including homologs thereof. Canine Flt-3 ligand protein can refer to a canine Flt-3 ligand, including homologs thereof, and feline Flt-3 ligand can refer to feline Flt-3 ligand, including homologs thereof. Canine CD40 can refer to a canine CD40, including homologs thereof; feline CD40 can refer to a feline CD40, including homologs thereof. Canine
20 CD154 can refer to a canine CD154, including homologs thereof; feline CD154 can refer to a feline CD154, including homologs thereof. Canine IL-5 can refer to canine IL-5, including homologs thereof; canine IL-13 can refer to canine IL-13, including homologs thereof. Feline IFN α can refer to a feline IFN α , including homologs thereof, and feline GM-CSF can refer to a feline GM-CSF, including homologs thereof. As used herein,
25 the phrase "regulate an immune response" refers to modulating the activity of cells or molecules involved in an immune response. The term "regulate" can refer to increasing or decreasing an immune response. Regulation of an immune response can be determined using methods known in the art as well as methods disclosed herein. The term, "immunoregulatory protein" refers to a protein that can modulate the activity of
30 cells or of molecules involved in an immune response. An immunoregulatory protein of the present invention refers to a canine IL-4, a canine and/or feline CD40, a canine

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and/or feline Flt3 ligand, a canine and/or feline CD154, a canine IL-5, a canine IL-13, a feline IFN α , and/or a feline GM-CSF protein as described herein. As used herein, the terms isolated canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF proteins and/or isolated canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF nucleic acid molecules refer to canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF proteins and/or canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF nucleic acid molecules derived from mammals and, as such, can be obtained from their natural source, or can be produced using, for example, recombinant nucleic acid technology or chemical synthesis. Also included in the present invention is the use of these proteins, nucleic acid molecules, antibodies, and/or compounds derived therefrom as therapeutic compositions to regulate the immune response of an animal as well as in other applications, such as those disclosed below.

One embodiment of the present invention is an isolated protein that includes a canine IL-4 protein, a canine and/or feline Flt-3 ligand protein, a canine and/or feline CD40 protein, a canine and/or feline CD154 protein, a canine interleukin-5 protein, a canine interleukin-13 protein, a feline interferon alpha protein, and/or a feline GM-CSF protein. It is to be noted that the term "a" or "an" entity refers to one or more of that entity; for example, a protein refers to one or more proteins or at least one protein. As such, the terms "a" (or "an"), "one or more" and "at least one" can be used interchangeably herein. It is also to be noted that the terms "comprising", "including", and "having" can be used interchangeably. According to the present invention, an isolated, or biologically pure, protein, is a protein that has been removed from its natural milieu. As such, "isolated" and/or "biologically pure" do not necessarily reflect the extent to which the protein has been purified. An isolated protein of the present invention can be obtained from its natural source, can be produced using recombinant

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DNA technology, or can be produced by chemical synthesis. Nucleic acid molecules of the present invention of known length isolated from *Canis familiaris* are denoted as follows: IL-4 is denoted as nCaIL-4_x, for example, nCaIL-4₅₄₉, wherein “#” refers to the number of nucleotides in that molecule; and in a similar fashion, Flt-3 ligand nucleic acid molecules are referred to as nCaFlt3L_x; CD40, nCaCD40_x; CD154, nCaCD154_x; IL-5, nCaIL-5_x; and IL-13, nCaIL-13_x. In a similar fashion, Flt-3 ligand nucleic acid molecules of the present invention of known length isolated from *Felis catus* are denoted as nFeFlt3L_x, CD40, nFeCD40_x; CD154, nFeCD154_x; IFN α , nFeIFN α _x; and GM-CSF (also denoted GMCSF), nFeGM-CSF_x. Similarly, proteins of the present invention of known length isolated from *Felis catus* are denoted as PFeFlt3L_x, PFeCD40_x, PFeCD154_x, PFeIFN α _x, and/or PFeGM-CSF_x; and proteins of the present invention of known length isolated from *Canis familiaris* are denoted PCaIL-4_x, PCaFlt3L_x, PCaCD40_x, PCaCD154_x, PCaIL-5_x, and/or PCaIL-13_x.

As used herein, an isolated canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, and/or feline GM-CSF ligand protein of the present invention (i.e., an canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF protein, respectively) can be a full-length protein or any homolog of such a protein. An isolated IL-4 protein of the present invention, including a homolog, can be identified in a straight-forward manner by the protein's ability to elicit an immune response against, (or to) an IL-4 protein, bind to an IL-4 receptor, stimulate B cell differentiation or activation or stimulate production of immunoglobulin by a B cell. An isolated Flt-3 ligand protein of the present invention, including a homolog, can be identified in a straight-forward manner by the protein's ability to elicit an immune response against a Flt-3 ligand protein, bind to Flt-3 receptor or stimulate Flt-3 receptor-bearing hematopoietic stem cells, early hematopoietic progenitor cells or immature lymphocytes. An isolated CD40 protein of the present invention, including a homolog, can be identified in a straight-forward manner by the protein's ability to elicit an immune response against a CD40 protein, bind to CD154 or stimulate CD154-bearing B cells, T cells, and/or epithelial cells. An isolated CD154 protein of the present invention,

including a homolog, can be identified in a straight-forward manner by the protein's ability to elicit an immune response to a CD154 protein, bind to CD40 or stimulate CD40-bearing B cells, T cells, and/or epithelial cells. An isolated IL-5 protein of the present invention, including a homolog, can be identified in a straight-forward manner

5 by the protein's ability to elicit an immune response to an IL-5 protein, bind to an IL-5 receptor, and/or stimulate eosinophils and/or cause thymocytes to produce cytotoxic T cells. An isolated IL-13 protein of the present invention, including a homolog, can be identified in a straight-forward manner by the protein's ability to elicit an immune response to an IL-13 protein, bind to an IL-13 receptor, and/or stimulate B cells, up-

10 regulate expression of MHC class II and/or CD23 on monocytes, macrophages and/or B cells; and/or inhibition of proinflammatory cytokines. An isolated interferon alpha protein of the present invention, including a homolog, can be identified in a straight-forward manner by the protein's ability to elicit an immune response to an interferon alpha protein, bind to an interferon-alpha receptor, and/or activate NK cells and/or

15 inhibit viral replication. An isolated GM-CSF protein of the present invention, including a homolog, can be identified in a straight-forward manner by the protein's ability to elicit an immune response to a GM-CSF protein, bind to a GM-CSF receptor, and/or activate granulocytes and/or macrophages. Examples of protein homologs of the present invention include immunoregulatory proteins of the present invention in which

20 amino acids have been deleted (e.g., a truncated version of the protein, such as a peptide), inserted, inverted, substituted and/or derivatized (e.g., by glycosylation, phosphorylation, acetylation, myristoylation, prenylation, palmitoylation, amidation and/or addition of glycerophosphatidyl inositol) such that the protein homolog includes at least one epitope capable of eliciting an immune response against the parent protein,

25 of binding to an antibody directed against the parent protein and/or of binding to the parent's receptor, where the term parent refers to the longer and/or full-length protein that the homolog is derived from. That is, when the homolog is administered to an animal as an immunogen, using techniques known to those skilled in the art, the animal will produce an immune response against at least one epitope of an immunoregulatory

30 protein of the present invention, depending upon which protein is administered to an animal. The ability of a protein to effect an immune response can be measured using

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techniques known to those skilled in the art. As used herein, the term "epitope" refers to the smallest portion of a protein capable of selectively binding to the antigen binding site of an antibody. It is well accepted by those skilled in the art that the minimal size of a protein epitope capable of selectively binding to the antigen binding site of an antibody
5 is about five or six to seven amino acids.

Homologs of immunoregulatory proteins of the present invention can be the result of natural allelic variation, including natural mutation. Protein homologs of the present invention can also be produced using techniques known in the art including, but not limited to, direct modifications to the protein and/or modifications to the gene
10 encoding the protein using, for example, classic or recombinant DNA techniques to effect random or targeted mutagenesis.

Immunoregulatory proteins of the present invention include variants of a full-length protein of a protein of the present invention. Such variants include proteins that are less than full-length. As used herein, variants of the present invention refer to
15 nucleic acid molecules that are naturally-occurring as defined below, and may result from alternative RNA splicing, alternative termination of an amino acid sequence or DNA recombination. Examples of variants include allelic variants as defined below. It is to be noted that a variant is an example of a homolog of the present invention.

Immunoregulatory proteins of the present invention are encoded by nucleic acid
20 molecules of the present invention. As used herein, an IL-4 nucleic acid molecule includes nucleic acid sequences related to a natural canine IL-4 gene. As used herein, a Flt-3 ligand nucleic acid molecule includes nucleic acid sequences related to a natural canine Flt-3 ligand gene. As used herein, a CD40 nucleic acid molecule includes nucleic acid sequences related to a natural CD40 gene. As used herein, a CD154 nucleic acid
25 molecule includes nucleic acid sequences related to a natural CD154 gene. As used herein, an IL-5 nucleic acid molecule includes nucleic acid sequences related to a natural IL-5 gene. As used herein, an IL-13 nucleic acid molecule includes nucleic acid sequences related to a natural IL-13 gene. As used herein, an IFN α nucleic acid molecule includes nucleic acid sequences related to a natural IFN α gene. As used
30 herein, a GM-CSF nucleic acid molecule includes nucleic acid sequences related to a natural GM-CSF gene. As used herein, a canine IL-4, a canine and/or feline CD40, a

canine and/or feline Flt3 ligand, a canine and/or feline CD154, a canine IL-5, a canine IL-13, a feline IFN α , and/or a feline GM-CSF gene refers to the natural genomic elements that encode an canine IL-4, a canine and/or feline CD40, a canine and/or feline Flt3 ligand, a canine and/or feline CD154, a canine IL-5, a canine IL-13, a feline IFN α ,
5 and/or a feline GM-CSF protein, respectively, and includes all regions such as regulatory regions that control production of the protein encoded by the gene (such as, but not limited to, transcription, translation or post-translation control regions) as well as the coding region itself, and any introns or non-translated coding regions. As used herein, a gene that "includes" or "comprises" a sequence may include that sequence in one
10 contiguous array, or may include the sequence as fragmented exons. As used herein, the term "coding region" refers to a continuous linear array of nucleotides that translates into a protein. A full-length coding region is that region that is translated into a full-length, i.e., a complete, protein as would be initially translated in its natural milieu, prior to any post-translational modifications.

15. In one embodiment, an IL-4 gene of the present invention includes the nucleic acid sequence SEQ ID NO:1, as well as the complement of SEQ ID NO:1. Nucleic acid sequence SEQ ID NO:1 represents the deduced sequence of the coding strand of a cDNA (complementary DNA) denoted herein as nucleic acid molecule nCaIL-4₅₄₉, the production of which is disclosed in the Examples. Nucleic acid molecule nCaIL-4₅₄₉
20 comprises an apparently full-length coding region of canine IL-4. The complement of SEQ ID NO:1 (represented herein by SEQ ID NO:3) refers to the nucleic acid sequence of the strand fully complementary to the strand having SEQ ID NO:1, which can easily be determined by those skilled in the art. Likewise, a nucleic acid sequence complement of any nucleic acid sequence of the present invention refers to the nucleic acid sequence
25 of the nucleic acid strand that is fully complementary to (i.e., can form a double helix with) the strand for which the sequence is cited. It should be noted that since nucleic acid sequencing technology is not entirely error-free, SEQ ID NO:1 (as well as other nucleic acid and protein sequences presented herein) represents an apparent nucleic acid sequence of the nucleic acid molecule encoding an immunoregulatory protein of the
30 present invention.

In another embodiment, a Flt-3 ligand gene of the present invention includes the nucleic acid sequence SEQ ID NO:6, as well as the complement represented by SEQ ID NO:8. Nucleic acid sequence SEQ ID NO:6 represents the deduced sequence of the coding strand of a cDNA denoted herein as nucleic acid molecule nCaFlt3L₁₀₁₃, the
5 production of which is disclosed in the Examples. Nucleic acid molecule nCaFlt3L₁₀₁₃ comprises an apparently full-length coding region of canine Flt-3 ligand.

In another embodiment, a Flt-3 ligand gene of the present invention includes the nucleic acid sequence SEQ ID NO:43, as well as the complement represented by SEQ ID NO:45. Nucleic acid sequence SEQ ID NO:43 represents the deduced sequence of the
10 coding strand of a cDNA denoted herein as nucleic acid molecule nFeFlt3L₉₄₂, the production of which is disclosed in the Examples. Nucleic acid molecule nFeFlt3L₉₄₂ comprises an apparently full-length coding region of feline Flt-3 ligand.

In another embodiment, a CD40 gene of the present invention includes the nucleic acid sequence SEQ ID NO:52, as well as the complement represented by SEQ ID
15 NO:54. Nucleic acid sequence SEQ ID NO:52 represents the deduced sequence of the coding strand of a cDNA denoted herein as nucleic acid molecule nCaCD40₁₄₂₅, the production of which is disclosed in the Examples. Nucleic acid molecule nCaCD40₁₄₂₅ comprises an apparently full-length coding region of canine CD40.

In another embodiment, a CD40 gene of the present invention includes the
20 nucleic acid sequence SEQ ID NO:60, as well as the complement represented by SEQ ID NO:62. Nucleic acid sequence SEQ ID NO:60 represents the deduced sequence of the coding strand of a cDNA denoted herein as nucleic acid molecule nFeCD40₃₃₆, the production of which is disclosed in the Examples. Nucleic acid molecule nFeCD40₃₃₆ comprises an apparent portion of the coding region of feline CD40.

25 In another embodiment, a CD154 gene of the present invention includes the nucleic acid sequence SEQ ID NO:64, as well as the complement represented by SEQ ID NO:66. Nucleic acid sequence SEQ ID NO:64 represents the deduced sequence of the coding strand of a cDNA denoted herein as nucleic acid molecule nCaCD154₁₈₇₈, the production of which is disclosed in the Examples. Nucleic acid molecule nCaCD154₁₈₇₈
30 comprises an apparently full-length coding region of canine CD154.

In another embodiment, a CD154 gene of the present invention includes the nucleic acid sequence SEQ ID NO:72, as well as the complement represented by SEQ ID NO:74. Nucleic acid sequence SEQ ID NO:72 represents the deduced sequence of the coding strand of a cDNA denoted herein as nucleic acid molecule nFeCD154₈₈₅, the
5 production of which is disclosed in the Examples. Nucleic acid molecule nFeCD154₈₈₅ comprises an apparently full-length coding region of feline CD154.

In another embodiment, an IL-5 gene of the present invention includes the nucleic acid sequence SEQ ID NO:80, as well as the complement represented by SEQ ID NO:82. Nucleic acid sequence SEQ ID NO:80 represents the deduced sequence of the
10 coding strand of a cDNA denoted herein as nucleic acid molecule nCaIL-5₆₁₀, the production of which is disclosed in the Examples. Nucleic acid molecule nCaIL-5₆₁₀ comprises an apparently full-length coding region of canine IL-5.

In another embodiment, an IL-13 gene of the present invention includes the nucleic acid sequence SEQ ID NO:91, as well as the complement represented by SEQ ID
15 NO:93. Nucleic acid sequence SEQ ID NO:91 represents the deduced sequence of the coding strand of a cDNA denoted herein as nucleic acid molecule nCaIL-13₁₃₀₂, the production of which is disclosed in the Examples. Nucleic acid molecule nCaIL-13₁₃₀₂ comprises an apparently full-length coding region of canine IL-13.

In another embodiment, an IFN α gene of the present invention includes the
20 nucleic acid sequence SEQ ID NO:107, as well as the complement represented by SEQ ID NO:109. Nucleic acid sequence SEQ ID NO:107 represents the deduced sequence of the coding strand of a cDNA denoted herein as nucleic acid molecule nFeIFN α _{567a}, the production of which is disclosed in the Examples. Nucleic acid molecule nFeIFN α _{567a} comprises an apparently full-length coding region of feline IFN α .

25 In another embodiment, a GM-CSF gene of the present invention includes the nucleic acid sequence SEQ ID NO:119, as well as the complement represented by SEQ ID NO:121. Nucleic acid sequence SEQ ID NO:119 represents the deduced sequence of the coding strand of a cDNA denoted herein as nucleic acid molecule nFeGM-CSF₄₄₄, the production of which is disclosed in the Examples. Nucleic acid molecule nFeGM-
30 CSF₄₄₄ comprises an apparently full-length coding region of feline GM-CSF.

Additional immunoregulatory nucleic acid molecules and proteins of the present invention having specific sequence identifiers are described in Table 1.

Table 1. Sequence identification numbers (SEQ ID NOs) and their corresponding nucleic acid molecules or proteins.

5	SEQ ID NO:	DESCRIPTION
	1	nCaIL-4 ₅₄₉ coding strand
	2	PCaIL-4 ₁₃₂
	3	nCaIL-4 ₅₄₉ complementary strand
	4	nCaIL-4 ₃₉₆ coding strand
10	5	nCaIL-4 ₃₉₆ complementary strand
	6	nCaFlt3L ₁₀₁₃ coding strand
	7	PCaFlt3L ₂₉₄
	8	nCaFlt3L ₁₀₁₃ complementary strand
	9	nCaFlt3L ₈₈₂ coding strand
15	10	nCaFlt3L ₈₈₂ complementary strand
	19	nCaIL-4 ₃₂₄ coding strand
	20	PCaIL-4 ₁₀₈
	21	nCaIL-4 ₃₂₄ complementary strand
	22	nCaFlt3L ₈₀₄ coding strand
20	23	PCaFlt3L ₂₆₈
	24	nCaFlt3L ₈₀₄ complementary strand
	25	nCaFlt3L ₉₈₅ coding strand
	26	PCaFlt3L ₂₇₆
	27	nCaFlt3L ₉₈₅ complementary strand
25	28	nCaFlt3L ₈₂₈ coding strand
	29	nCaFlt3L ₈₂₈ complementary strand
	30	nCaFlt3L ₇₅₀ coding strand
	31	PCaFlt3L ₂₅₀

SEQ ID NO:	DESCRIPTION
32	nCaFlt3L ₇₅₀ complementary strand
33	nCaFlt3L ₁₀₁₉ coding strand
34	PCaFlt3L ₃₁
35	nCaFlt3L ₁₀₁₉ complementary strand
36	nCaFlt3L ₉₃ coding strand
37	nCaFlt3L ₉₃ complementary strand
41	nFeFlt3L ₃₉₅ coding strand
42	nFeFlt3L ₇₉₃ coding strand
43	nFeFlt3L ₉₄₂ coding strand
44	PFeFlt3L ₂₉₁
45	nFeFlt3L ₉₄₂ complementary strand
46	nFeFlt3L ₈₇₃ coding strand
47	nFeFlt3L ₈₇₃ complementary strand
48	nFeFlt3L ₇₉₅ coding strand
49	PFeFlt3L ₂₆₅
50	nFeFlt3L ₇₉₅ complementary strand
51	nCaCD40 ₃₂₁ coding strand
52	nCaCD40 ₁₄₂₅ coding strand
53	PCaCD40 ₂₇₄
54	nCaCD40 ₁₄₂₅ complementary strand
55	nCaCD40 ₈₂₂ coding strand
56	nCaCD40 ₈₂₂ complementary strand
57	nCaCD40 ₇₆₅ coding strand
58	PCaCD40 ₂₅₅
59	nCaCD40 ₇₆₅ complementary strand
60	nFeCD40 ₃₃₆ coding strand
61	PFeCD40 ₁₁₂

SEQ ID NO:	DESCRIPTION
62	nFeCD40 ₃₃₆ complementary strand
63	nCaCD154 ₃₉₀ coding strand
64	nCaCD154 ₁₈₇₈ coding strand
65	PCaCD154 ₂₆₀
5 66	nCaCD154 ₁₈₇₈ complementary strand
67	nCaCD154 ₇₈₀ coding strand
68	nCaCD154 ₇₈₀ complementary strand
69	nCaCD154 ₆₃₃ coding strand
70	PCaCD154 ₂₁₁
10 71	nCaCD154 ₆₃₃ complementary strand
72	nFeCD154 ₈₈₅ coding strand
73	PFeCD154 ₂₆₀
74	nFeCD154 ₈₈₅ complementary strand
75	nFeCD154 ₇₈₀ coding strand
15 76	nFeCD154 ₇₈₀ complementary strand
77	nFeCD154 ₆₃₃ coding strand
78	PFeCD154 ₂₁₁
79	nFeCD154 ₆₃₃ complementary strand
80	nCaIL-5 ₆₁₀ coding strand
20 81	PCaIL-5 ₁₃₄
82	nCaIL-5 ₆₁₀ complementary strand
83	nCaIL-5 ₄₀₂ coding strand
84	nIL-5 ₄₀₂ complementary strand
85	nCaIL-5 ₃₄₅ coding strand
25 86	PCaIL-5 ₁₁₅
87	nCaIL-5 ₃₄₅ complementary strand
88	nCaIL-13 ₁₆₆ coding strand

SEQ ID NO.	DESCRIPTION
89	nCaIL-13 ₂₇₂ coding strand
90	nCaIL-13 ₂₇₈ coding strand
91	nCaIL-13 ₁₃₀₂ coding strand
92	PCaIL-13 ₁₃₁
5 93	nCaIL-13 ₁₃₀₂ complementary strand
94	nCaIL-13 ₃₉₃ coding strand
95	nCaIL-13 ₃₉₃ complementary strand
96	nCaIL-13 ₃₃₃ coding strand
97	PaIL-13 ₁₁₁
10 98	nCaIL-13 ₃₃₃ complementary strand
99	nCaIL-13 ₁₂₆₉ coding strand
100	PCaIL-13 ₁₃₀
101	nCaIL-13 ₁₂₆₉ complementary strand
102	nCaIL-13 ₃₉₀ coding strand
15 103	nCaIL-13 ₃₉₀ complementary strand
104	nCaIL-13 ₃₃₀ coding strand
105	PCaIL-13 ₁₁₀
106	nCaIL-13 ₃₃₀ complementary strand
107	nFeIFN α _{567a} coding strand
20 108	PFeIFN α _{189a}
109	nFeIFN α _{567a} complementary strand
110	nFeIFN α _{567b} coding strand
111	PFeIFN α _{189b}
112	nFeIFN α _{567b} complementary strand
25 113	nFeIFN α _{498a} coding strand
114	PFeIFN α _{166a}
115	nFeIFN α _{498a} complementary strand

SEQ ID NO:	DESCRIPTION
116	nFeFeIFN α_{498b} coding strand
117	PFeIFN α_{166b}
118	nFeIFN α_{498b} complementary strand
119	nFeGMCSF $_{444}$ coding strand
120	PFeGMCSF $_{144}$
121	nFeGMCSF $_{444}$ complementary strand
122	nFeGMCSF $_{432}$ coding strand
123	nFeGMCSF $_{432}$ complementary strand
124	nFeGMCSF $_{381}$ coding strand
125	PFeGMCSF $_{127}$
126	nFeGMCSF $_{381}$ complementary strand

In another embodiment, an IL-4 gene or nucleic acid molecule can be an allelic variant that includes a similar but not identical sequence to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:19, SEQ ID NO:21, and/or any other IL-4 nucleic acid sequence cited herein. In another embodiment, a Flt-3 ligand gene or nucleic acid molecule can be an allelic variant that includes a similar but not identical sequence to SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:50 and/or any other Flt-3 ligand nucleic acid sequence cited herein. In another embodiment, a CD40 gene or nucleic acid molecule can be an allelic variant that includes a similar but not identical sequence to SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:62 and/or any other CD40 nucleic acid sequence cited herein. In another embodiment, a CD154 gene or nucleic acid molecule can be an allelic variant that includes a similar but not identical sequence to SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:67,

SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:79 and/or any other CD154 nucleic acid sequence cited herein. In another embodiment, an IL-5 gene or nucleic acid molecule can be an allelic variant that includes a similar but not identical sequence to

5 SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:87 and/or any other IL-5 nucleic acid sequence cited herein. In another embodiment, an IL-13 gene or nucleic acid molecule can be an allelic variant that includes a similar but not identical sequence to SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID

10 NO:96, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:106 and/or any other IL-13 nucleic acid sequence cited herein. In another embodiment, an IFN α gene or nucleic acid molecule can be an allelic variant that includes a similar but not identical sequence to SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:113, SEQ ID

15 NO:115, SEQ ID NO:116, and/or SEQ ID NO:118 and/or any other IFN α nucleic acid sequence cited herein. In another embodiment, a GM-CSF gene or nucleic acid molecule can be an allelic variant that includes a similar but not identical sequence to SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, and/or SEQ ID NO:126 and/or any other GM-CSF nucleic acid cited herein. An allelic

20 variant of a canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF gene, including the particular SEQ ID NO's cited herein, is a gene that occurs at essentially the same locus (or loci) in the genome as the gene including the particular SEQ ID NO's cited herein, but which, due to natural variations

25 caused by, for example, mutation or recombination, has a similar but not identical sequence. Also included in the term allelic variant are allelic variants of cDNAs derived from such genes. Because natural selection typically selects against alterations that affect function, allelic variants usually encode proteins having similar activity to that of the protein encoded by the gene to which they are being compared. Allelic variants of

30 genes or nucleic acid molecules can also comprise alterations in the 5' or 3' untranslated regions of the gene (e.g., in regulatory control regions). can involve alternative

splicing of a nascent transcript, thereby bringing alternative exons into juxtaposition. Allelic variants are well known to those skilled in the art and would be expected to be found within a given animal, since the respective genomes are diploid, and sexual reproduction will result in the reassortment of alleles.

- 5 The minimal size of an canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF protein homolog of the present invention is a size sufficient to be encoded by a nucleic acid molecule capable of forming a stable hybrid (i.e., hybridize under stringent hybridization conditions) with the complementary
- 10 sequence of a nucleic acid molecule encoding the corresponding natural protein. Stringent hybridization conditions are determined based on defined physical properties of the gene to which the nucleic acid molecule is being hybridized, and can be defined mathematically. Stringent hybridization conditions are those experimental parameters that allow an individual skilled in the art to identify significant similarities between
- 15 heterologous nucleic acid molecules. These conditions are well known to those skilled in the art. See, for example, Sambrook, *et al.*, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Labs Press, and Meinkoth, *et al.*, 1984, *Anal. Biochem.* 138, 267-284. As explained in detail in the cited references, the determination of hybridization conditions involves the manipulation of a set of variables including the
- 20 ionic strength (M, in moles/liter), the hybridization temperature (°C), the concentration of nucleic acid helix destabilizing agents, such as formamide, the average length of the shortest hybrid duplex (n), and the percent G + C composition of the fragment to which an unknown nucleic acid molecule is being hybridized. For nucleic acid molecules of at least about 150 nucleotides, these variables are inserted into a standard mathematical
- 25 formula to calculate the melting temperature, or T_m , of a given nucleic acid molecule. As defined in the formula below, T_m is the temperature at which two complementary nucleic acid molecule strands will disassociate, assuming 100% complementarity between the two strands:

$$T_m = 81.5^{\circ}\text{C} + 16.6 \log M + 0.41(\%G + C) - 500/n - 0.61(\%\text{formamide}).$$

- 30 For nucleic acid molecules smaller than about 50 nucleotides, hybrid stability is defined by the dissociation temperature (T_d), which is defined as the temperature at which 50%

of the duplexes dissociate. For these smaller molecules, the stability at a standard ionic strength is defined by the following equation:

$$T_d = 4(G + C) + 2(A + T).$$

A temperature of 5°C below T_d is used to detect hybridization between perfectly
5 matched molecules.

Also well known to those skilled in the art is how base pair mismatch, i.e. differences between two nucleic acid molecules being compared, including non-complementarity of bases at a given location, and gaps due to insertion or deletion of one or more bases at a given location on either of the nucleic acid molecules being
10 compared, will affect T_m or T_d for nucleic acid molecules of different sizes. For example, T_m decreases about 1°C for each 1% of mismatched base pairs for hybrids greater than about 150 bp, and T_d decreases about 5°C for each mismatched base pair for hybrids below about 50 bp. Conditions for hybrids between about 50 and about 150 base pairs can be determined empirically and without undue experimentation using
15 standard laboratory procedures well known to those skilled in the art. These simple procedures allow one skilled in the art to set the hybridization conditions, by altering, for example, the salt concentration, the formamide concentration or the temperature, so that only nucleic acid hybrids with greater than a specified % base pair mismatch will hybridize. Stringent hybridization conditions are commonly understood by those skilled
20 in the art to be those experimental conditions that will allow about 30% base pair mismatch, i.e., about 70% identity. Because one skilled in the art can easily determine whether a given nucleic acid molecule to be tested is less than or greater than about 50 nucleotides, and can therefore choose the appropriate formula for determining hybridization conditions, he or she can determine whether the nucleic acid molecule will
25 hybridize with a given gene or specified nucleic acid molecule under stringent hybridization conditions and similarly whether the nucleic acid molecule will hybridize under conditions designed to allow a desired amount of base pair mismatch.

Hybridization reactions are often carried out by attaching the nucleic acid molecule to be hybridized to a solid support such as a membrane, and then hybridizing
30 with a labeled nucleic acid molecule, typically referred to as a probe, suspended in a hybridization solution. Examples of common hybridization reaction techniques include,

but are not limited to, the well-known Southern and northern blotting procedures. Typically, the actual hybridization reaction is done under non-stringent conditions, i.e., at a lower temperature and/or a higher salt concentration, and then high stringency is achieved by washing the membrane in a solution with a higher temperature and/or lower salt concentration in order to achieve the desired stringency.

Preferred portions, or fragments, of a canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF, protein of the present invention include at least 15 amino acids, at least 20 amino acids, at least 25 amino acids, at least 30 amino acids, at least 35 amino acids, at least 40 amino acids, at least 45 amino acids, at least 50 amino acids, at least 60 amino acids, at least 75 amino acids or at least 100 amino acids. An IL-4, IL-5, and/or IL-13 protein of the present invention can include at least a portion of an IL-4, IL-5, and/or IL-13 protein that is capable of binding to an IL-4, IL-5, and/or IL-13 receptor, respectively. IL-4, IL-5, and IL-13 receptors are known to those of skill in the art, and are described in Janeway et al., in *Immunobiology, the Immune System in Health and Disease*, Garland Publishing, Inc., NY, 1996. The IL-4, IL-5, and/or IL-13 receptor-binding portion of an IL-4, IL-5, and/or IL-13 protein, respectively, can be determined by incubating the protein with an isolated IL-4, IL-5, and/or IL-13 receptor, as appropriate, or a cell having an IL-4, IL-5, and/or IL-13 receptor on its surface, as appropriate. IL-4, IL-5, and/or IL-13 protein binding to purified IL-4, IL-5, and/or IL-13 receptor, respectively, can be determined using methods known in the art including Biacore® screening, confocal immunofluorescent microscopy, immunoprecipitation, gel chromatography, determination of inhibition of binding of antibodies that bind specifically to the IL-4, IL-5, and/or IL-13 binding domain of an IL-4, IL-5, and/or IL-13 receptor, ELISA using an IL-4, IL-5, and/or IL-13 receptor, respectively, labeled with a detectable tag such as an enzyme or chemiluminescent tag or yeast-2 hybrid technology. A Flt-3 ligand protein of the present invention can include at least a portion of a Flt-3 ligand protein that is capable of binding to Flt-3 receptor or stimulating Flt-3 receptor-bearing hematopoietic stem cells, early hematopoietic progenitor cells or immature lymphocytes. Flt-3 receptors are known to those of skill in the art, and are described in Drexler, *Leukemia*, vol. 10, pp. 588-599,

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1996. The Flt-3 receptor-binding portion of a Flt-3 ligand protein can be determined by incubating the protein with isolated Flt-3 receptor or a cell having a Flt-3 receptor on its surface. Flt-3 ligand protein binding to purified Flt-3 receptor can be determined using methods known in the art including Biacore® screening, confocal immunofluorescent microscopy, immunoprecipitation, gel chromatography, determination of inhibition of binding of antibodies that bind specifically to the Flt-3 ligand binding domain of a Flt-3 receptor, ELISA using a Flt-3 receptor labeled with a detectable tag such as an enzyme or chemiluminescent tag or yeast-2 hybrid technology. A CD40 and/or CD154 protein of the present invention can include at least a portion of a CD40 and/or CD154 protein that is capable of binding to a CD40 and/or CD154 receptor, respectively, or stimulating CD40 and/or CD154 receptor-bearing hematopoietic stem cells, early hematopoietic progenitor cells or immature lymphocytes. The CD40 and/or CD154 receptor-binding portion of a CD40 and/or CD154 protein can be determined by incubating the protein with isolated CD40 and/or CD154 receptor, as appropriate, or a cell having a CD40 and/or CD154 receptor on its surface, as appropriate. CD40 and/or CD154 protein binding to CD154 and/or CD40, respectively, can be determined using methods known in the art including Biacore® screening, confocal immunofluorescent microscopy, immunoprecipitation, gel chromatography, determination of inhibition of binding of antibodies that bind specifically to the CD40 and/or CD154 binding domain of CD40 and/or CD154, as appropriate, ELISA using a CD40 and/or CD154 labeled with a detectable tag such as an enzyme or chemiluminescent tag or yeast-2 hybrid technology.

The present invention also includes mimetopes of canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF proteins of the present invention. As used herein, a mimetope of an immunoregulatory protein of the present invention refers to any compound that is able to mimic the activity of such a canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF protein, respectively, often because the mimetope has a structure that mimics the particular protein. Mimetopes can be, but are not limited to: peptides that have been modified to decrease their susceptibility to degradation such as all-D retro peptides;

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anti-idiotypic and/or catalytic antibodies, or fragments thereof; non-proteinaceous immunogenic portions of an isolated protein (e.g., carbohydrate structures); and/or synthetic or natural organic molecules, including nucleic acids. Such mimetopes can be designed using computer-generated structures of proteins of the present invention.

- 5 Mimetopes can also be obtained by generating random samples of molecules, such as oligonucleotides, peptides or other organic molecules, and screening such samples by affinity chromatography techniques using the corresponding binding partner.

One embodiment of an immunoregulatory protein of the present invention is a fusion protein that includes either a canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF protein-containing domain, each attached to one or more fusion segments. Suitable fusion segments for use with the present invention include, but are not limited to, segments that can: link two or more immunoregulatory proteins of the present invention, to form multimeric forms of an immunoregulatory protein of the present invention; enhance a protein's stability; act as an immunopotentiator to enhance an immune response against an canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF protein; and/or assist in purification of an canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF protein (e.g., by affinity chromatography). A suitable fusion segment can be a domain of any size that has the desired function (e.g., imparts increased stability, imparts increased immunogenicity to a protein, and/or simplifies purification of a protein). Fusion segments can be joined to amino and/or carboxyl termini of the IL-4-containing domain, or the Flt-3 ligand-containing domain, or the CD40-containing domain, or the CD154-containing domain, or the IL-5-containing domain, or the IL-13-containing domain, or the IFN α -containing domain, or GM-CSF-containing domain, of a protein and can be susceptible to cleavage in order to enable straight-forward recovery of either canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF protein, respectively. Fusion

proteins are preferably produced by culturing a recombinant cell transformed with a fusion nucleic acid molecule that encodes a protein including the fusion segment attached to either the carboxyl and/or amino terminal end of an canine interleukin-4-, canine or feline Flt-3 ligand-, canine or feline CD40-, canine or feline CD154-, canine interleukin-5-, canine interleukin-13-, feline interferon alpha-, or feline GM-CSF-containing domain. Preferred fusion segments include a metal binding domain (e.g., a poly-histidine segment); an immunoglobulin binding domain (e.g., Protein A; Protein G; T cell; B cell; Fc receptor or complement protein antibody-binding domains); a sugar binding domain (e.g., a maltose binding domain); and/or a "tag" domain (e.g., at least a portion of -galactosidase, a strep tag peptide, a T7 tag peptide, a Flag™ peptide, or other domains that can be purified using compounds that bind to the domain, such as monoclonal antibodies). More preferred fusion segments include metal binding domains, such as a poly-histidine segment; a maltose binding domain; a strep tag peptide, such as that available from Biometra in Tampa, FL; and an S10 peptide.

15. A suitable fusion segment that links one IL-4 protein to another IL-4 protein, or one Flt-3 ligand protein to another Flt-3 ligand protein, or one CD40 protein to another CD40 protein, or one CD154 protein to another CD154 protein, or one IL-5 protein to another IL-5 protein to another IL-5 protein, or one IL-13 protein to another IL-13 protein, or one IFN α protein to another IFN α protein, or one GM-CSF protein to another GM-CSF protein, includes any amino acid sequence that enables such proteins to be linked while maintaining the biological function of either the canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF, proteins, respectively. Selection of a suitable linker is dependent upon how many proteins are to be linked to form one multimeric molecule and from where on either the canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF molecule the linker extends. Preferably, a linker fusion segment of the present invention comprises a peptide of from about 6 amino acid residues to about 40 residues, more preferably from about 6 residues to about 30 residues in length.

In another embodiment, an canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF protein of the present invention also includes at least one additional protein segment that is capable of targeting either canine
5 interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF protein, respectively, to a desired cell or receptive molecule. Such a multivalent targeting protein can be produced by culturing a cell transformed with a nucleic acid molecule comprising two or more nucleic acid domains joined together in
10 such a manner that the resulting nucleic acid molecule is expressed as a multivalent targeting protein containing a canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF protein or portion thereof and/or at least one targeting compound capable of delivering the canine interleukin-4, canine or feline Flt-3
15 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF protein, respectively, to a desired site in an animal.

Examples of multivalent targeting proteins include, but are not limited to, a canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
20 feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF protein of the present invention attached to one or more compounds that can bind to a receptive molecule on the surface of a cell located in an area of an animal where regulation of an immune response is desired. One of skill in the art can select appropriate targeting fusion segments depending upon the cell or receptive molecule
25 being targeted.

Another example of a multivalent protein of the present invention includes, but is not limited to, a canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF protein of the present invention attached to one or
30 more proteins that are potentially antigenic in mammals. Thus, immunogenicity of the

potentially antigenic protein could be enhanced by administering to a mammal together with an immunoregulatory protein of the present invention.

A naturally-occurring variant of a canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine
 5 interleukin-13, feline interferon alpha, or feline GM-CSF protein of the present invention is preferably isolated from (including isolation of the natural protein or production of the protein by recombinant or synthetic techniques) from mammals, including but not limited to dogs (i.e., canids), cats (i.e., felids), horses (i.e., equids), humans, cattle, chinchillas, ferrets, goats, mice, minks, rabbits, raccoons, rats, sheep,
 10 squirrels, swine, chickens, ostriches, quail and/or turkeys as well as other furry animals, pets, zoo animals, work animals and/or food animals. Particularly preferred animals from which to isolate canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF proteins are dogs, cats, horses and/or humans.

15 A preferred isolated protein of the present invention is a protein encoded by at least one of the following nucleic acid molecules: nCaIL-4₅₄₉, nCaIL-4₃₉₆, nCaIL-4₃₂₄, nCaFlt3L₁₀₁₃, nCaFlt3L₈₈₂, nCaFlt3L₈₀₄, nCaFlt3L₈₂₈, nCaFlt3L₉₈₅, nCaFlt3L₁₀₁₉, nCaFlt3L₉₃, nCaFlt3L₇₅₀, nFeFlt3L₃₉₅, nFeFlt3L₇₉₃, nFeFlt3L₉₄₂, nFeFlt3L₈₇₃, nFeFlt3L₇₉₅, nCaCD40₃₂₁, nCaCD40₁₄₂₅, nCaCD40₈₂₂, nCaCD40₇₆₅, nFeCD40₃₃₆, nCaCD154₃₉₀,
 20 nCaCD154₁₈₇₈, nCaCD154₇₈₀, nCaCD154₆₃₃, nFeCD154₈₈₅, nFeCD154₇₈₀, nFeCD154₆₃₃, nCaIL-5₆₁₀, nCaIL-5₄₀₂, nCaIL-5₃₄₅, nCaIL-13₁₆₆, nCaIL-13₂₇₂, nCaIL-13₂₇₈, nCaIL-13₁₃₀₂, nCaIL-13₃₉₃, nCaIL-13₃₃₃, nCaIL-13₁₂₆₉, nCaIL-13₃₉₀, nCaIL-13₃₃₀, nFeIFN α _{567a}, nFeIFN α _{567b}, nFeIFN α _{498a}, nFeIFN α _{498b}, nFeGMCSF₄₄₄, nFeGMCSF₄₃₂, nFeGMCSF₃₈₁ and/or allelic variants of any of these nucleic acid molecules. Also preferred is an
 25 isolated protein that is encoded by a nucleic acid molecule the having nucleic acid sequence SEQ ID NO:1, SEQ ID NO:4, SEQ ID NO:19, SEQ ID NO:6, SEQ ID NO:9, SEQ ID NO:22, SEQ ID NO:25, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:33, SEQ ID NO:36, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:55, SEQ ID NO:57, SEQ ID
 30 NO:60, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:72, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:80, SEQ ID NO:83, SEQ ID

NO:85, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:107, SEQ ID NO:110, SEQ ID NO:113, SEQ ID NO:116, SEQ ID NO:119, SEQ ID NO:122, SEQ ID NO:124; and/or an allelic variant of such a nucleic acid molecule.

5 Translation of SEQ ID NO:1, the coding strand of nCaIL-4₃₄₉, yields a protein of about 132 amino acids, denoted herein as PCaIL-4₁₃₂, the amino acid sequence of which is presented in SEQ ID NO:2, assuming an open reading frame having an initiation codon spanning from nucleotide 43 through nucleotide 45 of SEQ ID NO:1 and a stop codon spanning from nucleotide 439 through nucleotide 441 of SEQ ID NO:1.

10 Translation of SEQ ID NO:6, the coding strand of nCaFlt3L₁₀₁₃, yields a protein of about 294 amino acids, denoted herein as PCaFlt3L₂₉₄, the amino acid sequence of which is presented in SEQ ID NO:7, assuming an open reading frame having an initiation codon spanning from nucleotide 35 through nucleotide 37 of SEQ ID NO:6 and a stop codon spanning from nucleotide 917 through nucleotide 919 of SEQ ID
15 NO:6.

Translation of SEQ ID NO:43, the coding strand for nFeFlt3L₉₄₂, yields a protein of about 291 amino acids, denoted herein as PFeFlt3L₂₉₁, the amino acid sequence of which is presented in SEQ ID NO:44, assuming an open reading frame having an initiation codon spanning from nucleotide 31 through nucleotide 33 of SEQ ID NO:43
20 and a stop codon spanning from nucleotide 904 through nucleotide 906 of SEQ ID NO:43.

Translation of SEQ ID NO:52, the coding strand for nCaCD40₁₄₂₅, yields a protein of about 274 amino acids, denoted herein as PCaCD40₂₇₄, the amino acid sequence of which is presented in SEQ ID NO:53, assuming an open reading frame
25 having an initiation codon spanning from nucleotide 196 through nucleotide 198 of SEQ ID NO:52 and a stop codon spanning from about nucleotide 1018 through nucleotide 1020 of SEQ ID NO:52.

Translation of SEQ ID NO:60, the coding strand for nFeCD40₃₃₆, yields a protein of about 112 amino acids, denoted herein as PFeCD40₁₁₂, the amino acid sequence of
30 which is presented in SEQ ID NO:61, assuming an open reading frame having an initiation codon spanning from nucleotide 1 through nucleotide 3 of SEQ ID NO:60.

Translation of SEQ ID NO:64, the coding strand for nCaCD154₁₈₇₈, yields a protein of about 260 amino acids, denoted herein as PCaCD154₂₆₀, the amino acid sequence of which is presented in SEQ ID NO:65, assuming an open reading frame having an initiation codon spanning from nucleotide 284 through nucleotide 286 of SEQ ID NO:64 and a stop codon spanning from nucleotide 1064 through nucleotide 1066 of SEQ ID NO:64.

Translation of SEQ ID NO:72, the coding strand for nFeCD154₈₈₅, yields a protein of about 260 amino acids, denoted herein as PFeCD154₂₆₀, the amino acid sequence of which is presented in SEQ ID NO:73, assuming an open reading frame having an initiation codon spanning from nucleotide 29 through nucleotide 31 of SEQ ID NO:72, and a stop codon spanning from nucleotide 809 through nucleotide 811 of SEQ ID NO:72.

Translation of SEQ ID NO:80, the coding strand for nCaIL-5₆₁₀, yields a protein of about 134 amino acids, denoted herein as PCaIL-5₁₃₄, the amino acid sequence of which is presented in SEQ ID NO:81, assuming an open reading frame having an initiation codon spanning from nucleotide 29 through nucleotide 31 of SEQ ID NO:80, and a stop codon spanning from nucleotide 431 through nucleotide 433 of SEQ ID NO:80.

Translation of SEQ ID NO:91, the coding strand for nCaIL-13₁₃₀₂, yields a protein of about 131 amino acids, denoted herein as PCaIL-13₁₃₁, the amino acid sequence of which is presented in SEQ ID NO:92, assuming an open reading frame having an initiation codon spanning from nucleotide 52 through nucleotide 54 of SEQ ID NO:91 and a stop codon spanning from nucleotide 445 through nucleotide 447 of SEQ ID NO:91.

Translation of SEQ ID NO:107, the coding strand for nFeIFN α _{567a}, yields a protein of about 189 amino acids, denoted herein as PFeIFN α _{189a}, the amino acid sequence of which is presented in SEQ ID NO:108, assuming an open reading frame having an initiation codon spanning from nucleotide 1 through nucleotide 3 and a last codon prior to a stop codon spanning from nucleotide 565 through nucleotide 567 of SEQ ID NO:107.

Translation of SEQ ID NO:119, the coding strand for nFeGMCSF₄₄₄, yields a protein of about 144 amino acids, denoted herein as PFeGMCSF₁₄₄, the amino acid sequence of which is presented in SEQ ID NO:120, assuming an open reading frame having an initiation codon spanning from nucleotide 10 through nucleotide 12 of SEQ ID NO:119 and a stop codon spanning from nucleotide 442 through nucleotide 444 of SEQ ID NO:119.

Preferred IL-4 proteins of the present invention include proteins that are at least about 85%, preferably at least about 90%, and even more preferably at least about 95% identical to PCaIL-4₁₃₂, PCaIL-4₁₀₈, or fragments thereof. Preferred Flt-3 ligand proteins of the present invention include proteins that are at least about 75%, even more preferably at least about 80%, even more preferably at least about 85%, even more preferably at least about 90%, and even more preferably at least about 95% identical to PCaFlt3L₂₉₄, PCaFlt3L₂₆₈, PCaFlt3L₂₇₆, PCaFlt3L₂₅₀, PCaFlt3L₃₁, and/or fragments thereof. Additional preferred Flt-3 ligand proteins of the present invention includes proteins that are at least about 75%, even more preferably at least about 80%, even more preferably at least about 85%, even more preferably at least about 90%, and even more preferably at least about 95% identical to PFeFlt3L₂₉₁, PFeFlt3L₂₆₅ and/or fragments thereof. Preferred CD40 proteins of the present invention includes proteins that are at least about 70%, preferably at least about 75%, even more preferably at least about 80%, even more preferably at least about 85%, even more preferably at least about 90%, and even more preferably at least about 95% identical to PCaCD40₂₇₄, PCaCD40₂₅₅ and/or fragments thereof. Additional preferred CD40 proteins of the present invention includes proteins that are at least about 60%, at least about 65%, preferably at least about 70%, preferably at least about 75%, even more preferably at least about 80%, even more preferably at least about 85%, even more preferably at least about 90%, and even more preferably at least about 95% identical to PFeCD40₁₁₂ and/or fragments thereof. Preferred CD154 proteins of the present invention includes proteins that are at least about 80% identical, preferably at least about 85% identical, even more preferably at least about 90%, and even more preferably at least about 95% identical to PCaCD154₂₆₀, PCaCD154₂₁₁ and/or fragments thereof. Additional preferred CD154 proteins of the present invention includes proteins that are at least about ... % identical, even more

preferably at least about 90%, and even more preferably at least about 95% identical to PFeCD154₂₆₀, PFeCD154₂₁₁ and/or fragments thereof. Preferred IL-5 proteins of the present invention includes proteins that are at least about 85% identical, even more preferably at least about 90%, and even more preferably at least about 95% identical to

5 PCaIL-5₁₃₄, PCaIL-5₁₁₅ and/or fragments thereof. Preferred IL-13 proteins of the present invention includes proteins that are at least about 70% identical, preferably at least about 75% identical, more preferably at least about 80% identical, more preferably at least about 85% identical, even more preferably at least about 90%, and even more preferably at least about 95% identical to PCaIL-13₁₃₁, PCaIL-13₁₁₁, PCaIL-13₁₃₀, PCaIL-13₁₁₀,

10 and/or fragments thereof. Preferred IFN α proteins of the present invention include PFeIFN α _{189a}, PFeIFN α _{189b}, PFeIFN α _{166a}, and/or PFeIFN α _{166b}. Preferred GM-CSF proteins of the present invention include PFeGMCSF₁₄₄, and/or PFeGMCSF₁₂₇.

More preferred are IL-4 proteins comprising PCaIL-4₁₃₂, PCaIL-4₁₀₈, and/or proteins encoded by allelic variants of a nucleic acid molecule encoding proteins

15 PCaIL-4₁₃₂ and/or PCaIL-4₁₀₈. More preferred are Flt-3 ligand proteins comprising PCaFlt3L₂₉₄, PCaFlt3L₂₆₈, PCaFlt3L₂₇₆, PCaFlt3L₂₅₀, PCaFlt3L₃₁, PFeFlt3L₂₉₁, PFeFlt3L₂₆₅ and/or proteins encoded by allelic variants of a nucleic acid molecule encoding proteins PCaFlt3L₂₉₄, PCaFlt3L₂₆₈, PCaFlt3L₂₇₆, PCaFlt3L₂₅₀, PCaFlt3L₃₁, PFeFlt3L₂₉₁, and/or PFeFlt3L₂₆₅. More preferred are CD40 proteins comprising

20 PCaCD40₂₇₄, PCaCD40₂₅₅, and/or PFeCD40₁₁₂ and/or proteins encoded by allelic variants of a nucleic acid molecule encoding proteins PCaCD40₂₇₄, PCaCD40₂₅₅, and/or PFeCD40₁₁₂. More preferred are CD154 proteins comprising PCaCD154₂₆₀, PCaCD154₂₁₁, PFeCD154₂₆₀, PFeCD154₂₁₁ and/or proteins encoded by allelic variants of a nucleic acid molecule encoding one of proteins PCaCD154₂₆₀, PCaCD154₂₁₁,

25 PFeCD154₂₆₀, PFeCD154₂₁₁. More preferred are IL-5 proteins comprising PCaIL-5₁₃₄, PCaIL-5₁₁₅ and/or proteins encoded by allelic variants of a nucleic acid molecule encoding one of the proteins PCaIL-5₁₃₄ and/or PCaIL-5₁₁₅. More preferred are IL-13 proteins comprising PCaIL-13₁₃₁, PCaIL-13₁₁₁, PCaIL-13₁₃₀, PCaIL-13₁₁₀, and/or proteins encoded by allelic variants of a nucleic acid molecule encoding one of the proteins

30 PCaIL-13₁₃₁, PCaIL-13₁₁₁, PCaIL-13₁₃₀, PCaIL-13₁₁₀.

Also preferred are IL-4 proteins of the present invention having amino acid sequences that are at least about 85%, preferably at least about 90%, and even more preferably at least about 95% identical to SEQ ID NO:2, SEQ ID NO:20 and/or fragments thereof. Also preferred are Flt-3 ligand proteins of the present invention

5 having amino acid sequences that are at least about 75%, even more preferably at least about 80%, even more preferably at least about 85%, even more preferably at least about 90%, and even more preferably at least about 95% identical to SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, and/or SEQ ID NO:34 and/or fragments thereof. Additional preferred Flt-3 ligand proteins of the present invention includes

10 proteins that are at least about 75%, even more preferably at least about 80%, even more preferably at least about 85%, even more preferably at least about 90%, and/or even more preferably at least about 95% identical to SEQ ID NO:44, SEQ ID NO:49 and/or fragments thereof. Preferred CD40 proteins of the present invention includes proteins that are at least about 70%, preferably at least about 75%, even more preferably at least

15 about 80%, even more preferably at least about 85%, even more preferably at least about 90%, and/or even more preferably at least about 95% identical to SEQ ID NO:53, SEQ ID NO:58 and/or fragments thereof. Additional preferred CD40 proteins of the present invention includes proteins that are at least about 60%, at least about 65%, preferably at least about 70%, preferably at least about 75%, even more preferably at least about 80%,

20 even more preferably at least about 85%, even more preferably at least about 90%, and even more preferably at least about 95% identical to SEQ ID NO:61 and/or fragments thereof. Preferred CD154 proteins of the present invention includes proteins that are at least about 80% identical, preferably at least about 85% identical, even more preferably at least about 90%, and even more preferably at least about 95% identical to SEQ ID

25 NO:65, SEQ ID NO:70 and/or fragments thereof. Additional preferred CD154 proteins of the present invention includes proteins that are at least about 85% identical, even more preferably at least about 90%, and even more preferably at least about 95% identical to SEQ ID NO:73, SEQ ID NO:78 and/or fragments thereof. Preferred IL-5 proteins of the present invention includes proteins that are at least about 85% identical,

30 even more preferably at least about 90%, and even more preferably at least about 95% identical to SEQ ID NO:81, SEQ ID NO:86 and/or fragments thereof. Preferred IL-13

proteins of the present invention includes proteins that are at least about 70% identical, preferably at least about 75% identical, more preferably at least about 80% identical, more preferably at least about 85% identical, even more preferably at least about 90%, and even more preferably at least about 95% identical to SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, SEQ ID NO:105, and/or fragments thereof. Preferred IFN α proteins of the present invention include SEQ ID NO:108, SEQ ID NO:111, SEQ ID NO:114, SEQ ID NO:117. Preferred GM-CSF proteins of the present invention include SEQ ID NO:120, SEQ ID NO:125.

More preferred are IL-4 proteins comprising the amino acid sequence SEQ ID NO:2, SEQ ID NO:20; and/or IL-4 proteins encoded by allelic variants of nucleic acid molecules encoding IL-4 proteins having the amino acid sequence SEQ ID NO:2, SEQ ID NO:20. More preferred are Flt-3 ligand proteins comprising SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, and/or SEQ ID NO:34, SEQ ID NO:44, SEQ ID NO:49 and/or proteins encoded by allelic variants of a nucleic acid molecule encoding proteins SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, SEQ ID NO:34, SEQ ID NO:44, and/or SEQ ID NO:49. More preferred are CD40 proteins comprising SEQ ID NO:53, SEQ ID NO:58, SEQ ID NO:61 and/or proteins encoded by allelic variants of a nucleic acid molecule encoding proteins SEQ ID NO:53, SEQ ID NO:58 and/or SEQ ID NO:61. More preferred are CD154 proteins comprising SEQ ID NO:65, SEQ ID NO:70, SEQ ID NO:73, SEQ ID NO:78 and/or proteins encoded by allelic variants of a nucleic acid molecule encoding one of proteins SEQ ID NO:65, SEQ ID NO:70, SEQ ID NO:73, and/or SEQ ID NO:78. More preferred are IL-5 proteins comprising SEQ ID NO:81, SEQ ID NO:86 and/or proteins encoded by allelic variants of a nucleic acid molecule encoding one of the proteins SEQ ID NO:81, and/or SEQ ID NO:86. More preferred are IL-13 proteins comprising SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, SEQ ID NO:105, and/or proteins encoded by allelic variants of a nucleic acid molecule encoding one of the proteins SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, and/or SEQ ID NO:105.

Percent identities between amino acid or nucleic acid sequences can be determined using standard methods known to those of skill in the art. It is known in the art that methods to determine the percentage identity and the number of gaps are

substantially similar when different methods for determining sequence similarity are used and when the degree of similarity is greater than 30% amino acid identity, as described by Johnson et al., *J. Mol. Biol.*, vol. 233, pages 716-738, 1993, and Feng et al., *J. Mol. Evol.*, vol. 21, pages 112-125, 1985. Preferred methods to determine percentage identities between amino acid sequences and between nucleic acid sequences include comparisons using various computer programs such as GCG™ program (available from Genetics Computer Group, Madison, WI), DNAsis™ program (available from Hitachi Software, San Bruno, CA) or the MacVector™ program (available from the Eastman Kodak Company, New Haven, CT). Preferred settings for sequence comparisons using the DNAsis™ computer program or the GAP GCG™ program are disclosed herein in the Examples section.

Additional preferred IL-4 proteins of the present invention include proteins encoded by nucleic acid molecules comprising at least a portion of nCaIL-4₅₄₉, nCaIL-4₃₉₆, and/or nCaIL-4₃₂₄, as well as IL-4 proteins encoded by allelic variants of such nucleic acid molecules. Additional preferred Flt-3 ligand proteins of the present invention include proteins encoded by nucleic acid molecules comprising at least a portion of nCaFlt3L₁₀₁₃, nCaFlt3L₈₈₂, nCaFlt3L₈₀₄, nCaFlt3L₈₂₈, nCaFlt3L₉₈₅, nCaFlt3L₁₀₁₉, nCaFlt3L₉₃, nCaFlt3L₇₅₀, nFeFlt3L₃₉₅, nFeFlt3L₇₉₃, nFeFlt3L₉₄₂, nFeFlt3L₈₇₃, and/or nFeFlt3L₇₉₅ as well as Flt-3 ligand proteins encoded by allelic variants of such nucleic acid molecules. Additional preferred CD40 proteins of the present invention include proteins encoded by nucleic acid molecules encoding at least a portion of nCaCD40₃₂₁, nCaCD40₁₄₂₅, nCaCD40₈₂₂, nCaCD40₇₆₅, and/or nFeCD40₃₃₆ as well as CD40 proteins encoded by allelic variants of such nucleic acid molecules. Additional preferred CD154 proteins of the present invention include proteins encoded by nucleic acid molecules encoding at least a portion of nCaCD154₃₉₀, nCaCD154₁₈₇₈, nCaCD154₇₈₀, nCaCD154₆₃₃, nFeCD154₈₈₅, nFeCD154₇₈₀, and/or nFeCD154₆₃₃ as well as CD154 proteins encoded by allelic variants of such nucleic acid molecules. Additional preferred IL-5 proteins of the present invention include proteins encoded by nucleic acid molecules encoding at least a portion of nCaIL-5₆₁₀, nCaIL-5₄₀₂, and/or nCaIL-5₃₄₅ as well as IL-5 proteins encoded by allelic variants of such nucleic acid molecules. Additional preferred IL-13 proteins of the present invention include proteins encoded by

nucleic acid molecules encoding at least a portion of nCaIL-5₆₁₀, nCaIL-5₄₀₂, and/or nCaIL-5₃₄₅ as well as IL-13 proteins encoded by allelic variants of such nucleic acid molecules.

Also preferred are IL-4 proteins encoded by nucleic acid molecules having
5 nucleic acid sequences comprising at least a portion of SEQ ID NO:1, SEQ ID NO:4, and/or SEQ ID NO:19, as well as allelic variants of these nucleic acid molecules. Also preferred are Flt-3 ligand proteins encoded by nucleic acid molecules having nucleic acid sequences comprising at least a portion of SEQ ID NO:6, SEQ ID NO:9, SEQ ID NO:22, SEQ ID NO:25, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:33, SEQ ID
10 NO:36, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:46, and/or SEQ ID NO:48, as well as allelic variants of these nucleic acid molecules. Also preferred are CD40 proteins encoded by nucleic acid molecules having nucleic acid sequences comprising at least a portion of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:55, SEQ ID NO:57, and/or SEQ ID NO:60, as well as allelic variants of these nucleic acid
15 molecules. Also preferred are CD154 proteins encoded by nucleic acid molecules having nucleic acid sequences comprising at least a portion of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:72, SEQ ID NO:75, and/or SEQ ID NO:77, as well as allelic variants of these nucleic acid molecules. Also preferred are IL-5 proteins encoded by nucleic acid molecules having nucleic acid sequences
20 comprising at least a portion of SEQ ID NO:80, SEQ ID NO:83, and/or SEQ ID NO:85, as well as allelic variants of these nucleic acid molecules. Also preferred are IL-13 proteins encoded by nucleic acid molecules having nucleic acid sequences comprising at least a portion of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:102, and/or SEQ ID NO:104,
25 as well as allelic variants of these nucleic acid molecules.

Another embodiment of the present invention is a canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF nucleic acid molecule that includes one or more regulatory regions, full-length or partial coding regions, or
30 combinations thereof. The minimal size of a nucleic acid molecule of the present invention is a size sufficient to allow the formation of a stable hybrid (i.e., hybridization

under stringent hybridization conditions) with the complementary sequence of another nucleic acid molecule. As such, the minimal size of a canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF nucleic acid molecule
5 of the present invention is from about 12 to about 18 nucleotides in length.

In accordance with the present invention, an isolated nucleic acid molecule is a nucleic acid molecule that has been removed from its natural milieu (i.e., that has been subjected to human manipulation) and can include DNA, RNA, or derivatives of either DNA or RNA. As such, "isolated" does not reflect the extent to which the nucleic acid
10 molecule has been purified. An isolated canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF nucleic acid molecule of the present invention can be isolated from its natural source or produced using recombinant DNA technology (e.g., polymerase chain reaction (PCR) amplification or cloning) or
15 chemical synthesis. Isolated canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, and/or feline GM-CSF, nucleic acid molecules can include, for example, natural allelic variants and/or nucleic acid molecules modified by nucleotide insertions, deletions, substitutions, and/or inversions in a manner such that the
20 modifications do not substantially interfere with the nucleic acid molecule's ability to encode an canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, and/or feline GM-CSF protein of the present invention.

A canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40,
25 canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, and/or feline GM-CSF ligand nucleic acid molecule homolog can be produced using a number of methods known to those skilled in the art, see, for example, Sambrook et al., 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Labs Press; Sambrook et al., *ibid*. For example, nucleic acid molecules can be modified
30 using a variety of techniques including, but not limited to, classic mutagenesis and recombinant DNA techniques such as site-directed mutagenesis, chemical treatment,

restriction enzyme cleavage, ligation of nucleic acid fragments, PCR amplification, synthesis of oligonucleotide mixtures and ligation of mixture groups to "build" a mixture of nucleic acid molecules, and combinations thereof. Nucleic acid molecule homologs can be selected by hybridization with either a canine interleukin-4, canine or
5 feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF nucleic acid molecule or by screening the function of a protein encoded by the nucleic acid molecule (e.g., ability to elicit an immune response against at least one epitope of a canine interleukin-4,
10 canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF protein, respectively).

An isolated nucleic acid molecule of the present invention can include a nucleic acid sequence that encodes at least one canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine
15 interleukin-13, feline interferon alpha, or feline GM-CSF protein of the present invention, examples of such proteins being disclosed herein. Although the phrase "nucleic acid molecule" primarily refers to the physical nucleic acid molecule and the phrase "nucleic acid sequence" primarily refers to the sequence of nucleotides on the nucleic acid molecule, the two phrases can be used interchangeably, especially with
20 respect to a nucleic acid molecule, or a nucleic acid sequence, being capable of encoding a canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF ligand protein.

A preferred nucleic acid molecule of the present invention, when administered to
25 an animal, is capable of regulating an immune response in an animal. As will be disclosed in more detail below, such a nucleic acid molecule can be, or encode, an antisense RNA, a molecule capable of triple helix formation, a ribozyme, or other nucleic acid-based drug compound. In additional embodiments, a nucleic acid molecule of the present invention can encode an immunoregulatory protein (e.g., a cell-bound or
30 soluble protein of the present invention), the nucleic acid molecule being delivered to the

animal, for example, by direct injection (i.e., as a genetic vaccine) or in a vehicle such as a recombinant virus vaccine or a recombinant cell vaccine.

One embodiment of the present invention is an IL-4 nucleic acid molecule comprising all or part (i.e., a fragment of the IL-4 nucleic acid molecule) of nucleic acid molecules nCaIL-4₅₄₉, nCaIL-4₃₉₆, and/or nCaIL-4₃₂₄, or allelic variants of these nucleic acid molecules. One embodiment of the present invention is a Flt-3 ligand nucleic acid molecule comprising all or part (i.e., a fragment of the Flt-3 ligand nucleic acid molecule) of nucleic acid molecules nCaFlt3L₁₀₁₃, nCaFlt3L₈₈₂, nCaFlt3L₈₀₄, nCaFlt3L₈₂₈, nCaFlt3L₉₈₅, nCaFlt3L₁₀₁₉, nCaFlt3L₉₃, nCaFlt3L₇₅₀, nFeFlt3L₃₉₅, nFeFlt3L₇₉₃, nFeFlt3L₉₄₂, nFeFlt3L₈₇₃, and/or nFeFlt3L₇₉₅ and/or allelic variants of these nucleic acid molecules. One embodiment of the present invention is a CD40 nucleic acid molecule comprising all or part (i.e. a fragment of the CD40 nucleic acid molecule) of nucleic acid molecules nCaCD40₃₂₁, nCaCD40₁₄₂₅, nCaCD40₈₂₂, nCaCD40₇₆₅, and/or nFeCD40₃₃₆ and/or allelic variants of these nucleic acid molecules. One embodiment of the present invention is a CD154 nucleic acid molecule comprising all or part of nucleic acid molecules nCaCD154₃₉₀, nCaCD154₁₈₇₈, nCaCD154₇₈₀, nCaCD154₆₃₃, nFeCD154₈₈₅, nFeCD154₇₈₀, and/or nFeCD154₆₃₃, and/or allelic variants of these nucleic acid molecules. One embodiment of the present invention is an IL-5 nucleic acid molecule comprising all or part of nucleic acid molecules nCaIL-5₆₁₀, nCaIL-5₄₀₂, and/or nCaIL-5₃₄₅, and/or allelic variants of these nucleic acid molecules. One embodiment of the present invention is an IL-13 nucleic acid molecule comprising all or part of nucleic acid molecules nCaIL-13₁₆₆, nCaIL-13₂₇₂, nCaIL-13₂₇₈, nCaIL-13₁₃₀₂, nCaIL-13₃₉₃, nCaIL-13₃₃₃, nCaIL-13₁₂₆₉, nCaIL-13₃₉₀, and/or nCaIL-13₃₃₀, and/or allelic variants of these nucleic acid molecules. Another preferred nucleic acid molecule of the present invention includes at least a portion of (i.e., a fragment of the nucleic acid molecule) nucleic acid sequence SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID

NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, and/or SEQ ID NO:126, as well as allelic variants of nucleic acid molecules having these nucleic acid sequences. Such nucleic acid molecules can include nucleotides in addition to those included in the SEQ ID NOs, such as, but not limited to, a full-length gene, a full-length coding region, a nucleic acid molecule encoding a fusion protein, and/or a nucleic acid molecule encoding a multivalent therapeutic compound.

One embodiment of an isolated nucleic acid molecule of the present invention is a nucleic acid molecule that can be any of the following: (a) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:19, and/or SEQ ID NO:21 and/or a homolog thereof, wherein said homolog has an at least 50 contiguous nucleotide region identical in sequence to a 50 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:19, and/or SEQ ID NO:21; (b) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:36, and/or SEQ ID NO:37, and/or a homolog thereof, wherein said homolog has an at least 40 contiguous nucleotide region identical in sequence to a 40 contiguous nucleotide region

of a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:36, and/or SEQ ID NO:37; (c) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, and/or SEQ ID NO:50, and/or a homolog thereof, wherein said homolog has an at least 30 contiguous nucleotide region identical in sequence to a 30 contiguous nucleotide region of a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, and/or SEQ ID NO:50; (d) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, and/or SEQ ID NO:59, and/or a homolog thereof, wherein said homolog has an at least 40 contiguous nucleotide region identical in sequence to a 40 contiguous nucleotide region of a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, and/or SEQ ID NO:59; (e) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:60 and/or SEQ ID NO:62, and/or a homolog thereof, wherein said homolog has an at least 30 contiguous nucleotide region identical in sequence to a 30 contiguous nucleotide region of a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:60 and/or SEQ ID NO:62; (f) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69 and/or SEQ ID NO:71, and/or a homolog thereof, wherein said homolog has an at least 45 contiguous nucleotide region identical in sequence to a 45 contiguous nucleotide region of a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69 and/or

SEQ ID NO:71; (g) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, and/or SEQ ID NO:79, and/or a homolog thereof, wherein said homolog has an at least 35 contiguous nucleotide region identical in sequence to a 35 contiguous nucleotide region of a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, and/or SEQ ID NO:79; (h) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, and/or SEQ ID NO:87, and/or a homolog thereof, wherein said homolog has an at least 45 contiguous nucleotide region identical in sequence to a 45 contiguous nucleotide region of a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, and/or SEQ ID NO:87; (i) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, and/or SEQ ID NO:106, and/or a homolog thereof, wherein said homolog has an at least 15 contiguous nucleotide region identical in sequence to a 15 contiguous nucleotide region of a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, and/or SEQ ID NO:106; (j) an isolated nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:116, and/or SEQ ID NO:118; and/or (k) an isolated nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, and/or SEQ ID NO:126. The phrase, a homolog having an at least "x" contiguous nucleotide region identical in sequence to an "x" contiguous

nucleotide region of a nucleic acid molecule selected from the group consisting of SEQ ID NO: "y", refers to an "x"-nucleotide in length nucleic acid molecule that is identical in sequence to an "x"-nucleotide portion of SEQ ID NO: "y", as well as to nucleic acid molecules that are longer in length than "x". The additional length may be in the form of nucleotides that extend from either the 5' or the 3' end(s) of the contiguous identical "x"-nucleotide portion. The 5' and/or 3' extensions can include one or more extensions that have no identity to an immunoregulatory molecule of the present invention, as well as extensions that show similarity or identity to cited nucleic acids sequences or portions thereof.

10 In another embodiment, an isolated nucleic acid molecule of the present invention can be any of the following: (a) a nucleic acid molecule having a nucleic acid sequence encoding an IL-4 protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 85 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:2 and/or SEQ ID
15 NO:20 and/or (ii) a protein comprising a fragment of at least 20 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:2 and/or SEQ ID NO:20; (b) a nucleic acid molecule having a nucleic acid sequence encoding a Flt-3 ligand protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 75 percent identical to an amino acid sequence selected
20 from the group consisting of SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, and/or SEQ ID NO:34, and/or (ii) a protein comprising a fragment of at least 25 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, and/or SEQ ID NO:34; (c) a nucleic acid molecule having a nucleic acid sequence encoding a Flt-3 ligand protein
25 selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 75 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:44 and/or SEQ ID NO:49 and/or (ii) a protein comprising a fragment of at least 25 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:44 and/or SEQ ID NO:49; (d) a nucleic acid molecule having
30 a nucleic acid sequence encoding a CD40 protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 70 percent identical to

an amino acid sequence selected from the group consisting of SEQ ID NO:53 and/or SEQ ID NO:58 and/or (ii) a protein comprising a fragment of at least 30 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:53 and/or SEQ ID NO:58; (e) a nucleic acid molecule having a nucleic acid sequence encoding a

5 CD40 protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 60 percent identical to an amino acid sequence comprising SEQ ID NO:61 and/or (ii) a protein comprising a fragment of at least 20 amino acids of an amino acid sequence comprising SEQ ID NO:61; (f) a nucleic acid molecule having a nucleic acid sequence encoding a CD154 protein selected from the group consisting of

10 (i) a protein having an amino acid sequence that is at least about 80 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:65 and/or SEQ ID NO:70, and/or (ii) a protein comprising a fragment of at least 35 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:65 and/or SEQ ID NO:70; (g) a nucleic acid molecule having a nucleic acid sequence encoding a

15 CD154 protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 85 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:73 and/or SEQ ID NO:78, and/or (ii) a protein comprising a fragment of at least 50 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:73 and/or SEQ ID NO:78; (h) a nucleic acid

20 molecule having a nucleic acid sequence encoding an IL-5 protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 85 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:81 and/or SEQ ID NO:86 and/or (ii) a protein comprising a fragment of at least 20 amino acids of an amino acid sequence selected from the group consisting of SEQ ID

25 NO:81 and/or SEQ ID NO:86; (i) a nucleic acid molecule having a nucleic acid sequence encoding an IL-13 protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 70 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, and/or SEQ ID NO:105 and/or (ii) a protein comprising a fragment of

30 at least 15 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, and/or SEQ ID NO:105; (j) a nucleic

acid molecule having a nucleic acid sequence encoding an interferon alpha protein having an amino acid sequence that is selected from the group consisting of amino acid sequence SEQ ID NO:108, SEQ ID NO:111, SEQ ID NO:114, and/or SEQ ID NO:117; (k) a nucleic acid molecule having a nucleic acid sequence encoding a GMCSF protein having an amino acid sequence that is selected from the group consisting of amino acid sequence SEQ ID NO:120, SEQ ID NO:125, and/or (l) a nucleic acid molecule comprising a complement of any of the before-mentioned nucleic acid sequences; wherein said IL-4 protein elicits an immune response against an IL-4 protein selected from the group consisting of SEQ ID NO:2 and/or SEQ ID NO:20 and/or is a protein with interleukin-4 activity, said Flt-3 ligand protein elicits an immune response against a Flt-3 ligand protein selected from the group consisting of SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, SEQ ID NO:34, SEQ ID NO:44, and/or SEQ ID NO:49 and/or is a protein with Flt-3 ligand activity, said CD40 protein elicits an immune response against a CD40 protein selected from the group consisting of SEQ ID NO:53, SEQ ID NO:58, and/or SEQ ID NO:61 and/or is a protein with CD40 activity, said CD154 protein elicits an immune response against a CD154 protein selected from the group consisting of SEQ ID NO:65, SEQ ID NO:70, SEQ ID NO:73, and/or SEQ ID NO:78 and/or is a protein with CD154 activity, said IL-5 protein elicits an immune response against a IL-5 protein selected from the group consisting of SEQ ID NO:81 and/or SEQ ID NO:86 and/or is a protein with IL-5 activity, said IL-13 protein elicits an immune response against an IL-13 protein selected from the group consisting of SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, and/or SEQ ID NO:105 and/or is a protein with IL-13 activity, said interferon alpha protein elicits an immune response against an interferon alpha protein selected from the group consisting of SEQ ID NO:108, SEQ ID NO:111, SEQ ID NO:114, and/or SEQ ID NO:117 and/or is a protein with interferon alpha activity, and said GMCSF protein elicits an immune response against a GMCSF protein selected from the group consisting of SEQ ID NO:120 and/or SEQ ID NO:125 and/or is a protein with GM-CSF activity.

In one embodiment, an IL-4 nucleic acid molecule of the present invention encodes a protein that is at least about 85%, preferably at least about 90%, preferably at least about 92%, and even more preferably at least about 95% identical to PCaIL-4₁₃₂

and/or PCaIL-4₁₀₈. In one embodiment, a Flt-3 ligand nucleic acid molecule of the present invention encodes a protein that is at least about 75%, even more preferably at least about 80%, even more preferably at least about 85%, even more preferably at least about 90%, and even more preferably at least about 95% identical to PCaFlt3L₂₉₄,
5 PCaFlt3L₂₆₈, PCaFlt3L₂₇₆, PCaFlt3L₂₅₀, and/or PCaFlt3L₃₁. In one embodiment, a Flt-3 ligand nucleic acid molecule of the present invention encodes a protein that is at least about 75%, more preferably at least about 80%, even more preferably at least about 85%, even more preferably at least about 90%, and even more preferably at least about 95% identical to PFeFlt3L₂₉₁, and/or PFeFlt3L₂₆₅. In one embodiment, a CD40 nucleic acid
10 molecule of the present invention encodes a protein that is at least about PCaCD40₂₇₄, and/or PCaCD40₂₅₅. In one embodiment, a CD40 nucleic acid molecule of the present invention encodes a protein that is at least about 60%, preferably at least about 65%, preferably at least about 70%, preferably at least about 75%, even more preferably at least about 80%, even more preferably at least about 85%, even more preferably at least
15 about 90%, and even more preferably at least about 95% identical to PFeCD40₁₁₂. In one embodiment, a CD154 nucleic acid molecule of the present invention encodes a protein that is at least about 80%, at least about 85%, more preferably at least about 90%, and even more preferably at least about 95% identical to PCaCD154₂₆₀, and/or PCaCD154₂₁₁. In one embodiment, a CD154 nucleic acid molecule of the present
20 invention encodes a protein that is at least about 85%, more preferably at least about 90%, and even more preferably at least about 95% identical to PFeCD154₂₆₀, PFeCD154₂₁₁. In one embodiment, an IL-5 nucleic acid molecule of the present invention encodes a protein that is at least about 85%, more preferably at least about 90%, and even more preferably at least about 95% identical to PCaIL-5₁₃₄, and/or PCaIL-
25 5₁₁₅. In one embodiment, an IL-13 nucleic acid molecule of the present invention encodes a protein that is at least about 70%, at least about 75%, at least about 80%, preferably at least about 85%, more preferably at least about 90%, and even more preferably at least about 95% identical to PCaIL-13₁₃₁, PCaIL-13₁₁₁, PCaIL-13₁₃₀, PCaIL-13₁₁₀. Even more preferred is a nucleic acid molecule encoding PCaIL-4₁₃₂, PCaIL-4₁₀₈,
30 PCaFlt3L₂₉₄, PCaFlt3L₂₆₈, PCaFlt3L₂₇₆, PCaFlt3L₂₅₀, PCaFlt3L₃₁, PFeFlt3L₂₉₁, PFeFlt3L₂₆₅, PCaCD40₂₇₄, PCaCD40₂₅₅, PFeCD40₁₁₂, PCaCD154₂₆₀, PCaCD154₂₁₁,

PFeCD154₂₆₀, PFeCD154₂₁₁, PCaIL-5₁₃₄, PCaIL-5₁₁₅, PCaIL-13₁₃₁, PCaIL-13₁₁₁, PCaIL-13₁₃₀, PCaIL-13₁₁₀ and/or an allelic variant of such a nucleic acid molecule.

In another embodiment, an IL-4 nucleic acid molecule of the present invention encodes a protein having an amino acid sequence that is at least about 85%, preferably at least about 90%, and even more preferably at least about 95% identical to SEQ ID NO:2, SEQ ID NO:20. The present invention also includes an IL-4 nucleic acid molecule encoding a protein having at least a portion of SEQ ID NO:2, and/or SEQ ID NO:20, as well as allelic variants of an IL-4 nucleic acid molecule encoding a protein having these sequences, including nucleic acid molecules that have been modified to accommodate codon usage properties of the cells in which such nucleic acid molecules are to be expressed.

In another embodiment, a Flt-3 ligand nucleic acid molecule of the present invention encodes a protein having an amino acid sequence that is at least about 75%, even more preferably at least about 80%, even more preferably at least about 85%, even more preferably at least about 90%, and even more preferably at least about 95% identical to SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, and/or SEQ ID NO:34. The present invention also includes a Flt-3 ligand nucleic acid molecule encoding a protein having at least a portion of SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, and/or SEQ ID NO:34, as well as allelic variants of a Flt-3 ligand nucleic acid molecule encoding a protein having these sequences, including nucleic acid molecules that have been modified to accommodate codon usage properties of the cells in which such nucleic acid molecules are to be expressed.

In another embodiment, a Flt-3 ligand nucleic acid molecule of the present invention encodes a protein having an amino acid sequence that is at least about 75%, more preferably at least about 80%, even more preferably at least about 85%, even more preferably at least about 90%, and even more preferably at least about 95% identical to SEQ ID NO:44, and/or SEQ ID NO:49. The present invention also includes a Flt-3 ligand nucleic acid molecule encoding a protein having at least a portion of SEQ ID NO:44, and/or SEQ ID NO:49, as well as allelic variants of a Flt-3 ligand nucleic acid molecule encoding a protein having these sequences, including nucleic acid molecules

that have been modified to accommodate codon usage properties of the cells in which such nucleic acid molecules are to be expressed.

In another embodiment, a CD40 nucleic acid molecule of the present invention encodes a protein having an amino acid sequence that is at least about 70%, preferably
5 at least about 75%, even more preferably at least about 80%, even more preferably at least about 85%, even more preferably at least about 90%, and even more preferably at least about 95% identical to SEQ ID NO:53 and/or SEQ ID NO:58. The present invention also includes a CD40 nucleic acid molecule encoding a protein having at least a portion of SEQ ID NO:53 and/or SEQ ID NO:58, as well as allelic variants of a CD40
10 nucleic acid molecule encoding a protein having these sequences, including nucleic acid molecules that have been modified to accommodate codon usage properties of the cells in which such nucleic acid molecules are to be expressed.

In another embodiment, a CD40 nucleic acid molecule of the present invention encodes a protein having an amino acid sequence that is at least about 60%, preferably at
15 least about 65%, preferably at least about 70%, preferably at least about 75%, even more preferably at least about 80%, even more preferably at least about 85%, even more preferably at least about 90%, and even more preferably at least about 95% identical to SEQ ID NO:60. The present invention also includes a CD40 nucleic acid molecule encoding a protein having at least a portion of SEQ ID NO:60, as well as allelic variants
20 of a CD40 nucleic acid molecule encoding a protein having these sequences, including nucleic acid molecules that have been modified to accommodate codon usage properties of the cells in which such nucleic acid molecules are to be expressed.

In another embodiment, a CD154 nucleic acid molecule of the present invention encodes a protein having an amino acid sequence that is at least about at least about
25 80%, at least about 85%, more preferably at least about 90%, and even more preferably at least about 95% identical to SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:67, and/or SEQ ID NO:69. The present invention also includes a CD154 nucleic acid molecule encoding a protein having at least a portion of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:67, and/or SEQ ID NO:69, as well as allelic variants of a CD154 nucleic acid
30 molecule encoding a protein having these sequences, including nucleic acid molecules

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that have been modified to accommodate codon usage properties of the cells in which such nucleic acid molecules are to be expressed.

In another embodiment, a CD154 nucleic acid molecule of the present invention encodes a protein having an amino acid sequence that is at least about at least about
5 85%, more preferably at least about 90%, and even more preferably at least about 95% identical to SEQ ID NO:72, SEQ ID NO:75, and/or SEQ ID NO:77. The present invention also includes a CD154 nucleic acid molecule encoding a protein having at least a portion of SEQ ID NO:72, SEQ ID NO:75, and/or SEQ ID NO:77, as well as allelic variants of a CD154 nucleic acid molecule encoding a protein having these
10 sequences, including nucleic acid molecules that have been modified to accommodate codon usage properties of the cells in which such nucleic acid molecules are to be expressed.

In another embodiment, an IL-5 nucleic acid molecule of the present invention encodes a protein having an amino acid sequence that is at least about at least about
15 85%, at least about 85%, more preferably at least about 90%, and even more preferably at least about 95% identical to SEQ ID NO:80, SEQ ID NO:83, and/or SEQ ID NO:85. The present invention also includes an IL-5 nucleic acid molecule encoding a protein having at least a portion of SEQ ID NO:80, SEQ ID NO:83, and/or SEQ ID NO:85, as well as allelic variants of an IL-5 nucleic acid molecule encoding a protein having these
20 sequences, including nucleic acid molecules that have been modified to accommodate codon usage properties of the cells in which such nucleic acid molecules are to be expressed.

In another embodiment, an IL-13 nucleic acid molecule of the present invention encodes a protein having an amino acid sequence that is at least about at least about
25 70%, at least about 75%, at least about 80%, preferably at least about 85%, more preferably at least about 90%, and even more preferably at least about 95% identical to SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:102, and/or SEQ ID NO:104. The present invention also includes an IL-13 nucleic acid molecule encoding a protein having at least
30 a portion of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:102, and/or SEQ ID NO:104, as

well as allelic variants of an IL-13 nucleic acid molecule encoding a protein having these sequences, including nucleic acid molecules that have been modified to accommodate codon usage properties of the cells in which such nucleic acid molecules are to be expressed.

- 5 In one embodiment, an IL-4 nucleic acid molecule of the present invention is at least about 90%, and preferably at least about 95% identical to nCaIL-4₅₄₉. Even more preferred is a nucleic acid molecule comprising nCaIL-4₅₄₉, nCaIL-4₃₉₆, nCaIL-4₃₂₄, and/or an allelic variant of such a nucleic acid molecule. In another embodiment, a Flt-3 ligand nucleic acid molecule of the present invention is at least about 75%, more
- 10 preferably at least about 80%, more preferably at least about 85%, more preferably at least about 90% and even more preferably at least about 95% identical to nCaFlt3L₁₀₁₃. Even more preferred is a nucleic acid molecule comprising nCaFlt3L₁₀₁₃, nCaFlt3L₈₈₂, nCaFlt3L₈₀₄, nCaFlt3L₈₂₈, nCaFlt3L₉₈₅, nCaFlt3L₁₀₁₉, nCaFlt3L₉₃, and/or nCaFlt3L₇₅₀, and/or an allelic variant of such a nucleic acid molecule. In one embodiment, a Flt-3
- 15 ligand nucleic acid molecule of the present invention is at least about 75%, more preferably at least about 80%, more preferably at least about 85%, more preferably at least about 90% and even more preferably at least about 95% identical to nFeFlt3L₉₄₂. Even more preferred is a nucleic acid molecule comprising nFeFlt3L₃₉₅, nFeFlt3L₇₉₃, nFeFlt3L₉₄₂, nFeFlt3L₈₇₃, and/or nFeFlt3L₇₉₅, and/or an allelic variant of such a nucleic
- 20 acid molecule. In one embodiment, a CD40 nucleic acid molecule of the present invention is at least about 70%, at least about 75%, more preferably at least about 80%, more preferably at least about 85%, more preferably at least about 90% and even more preferably at least about 95% identical to nCaCD40₃₂₁, nCaCD40₁₄₂₅, nCaCD40₈₂₂, and/or nCaCD40₇₆₅, and/or an allelic variant of such a nucleic acid molecule. In one
- 25 embodiment, a CD40 nucleic acid molecule of the present invention is at least about 70%, at least about 75%, more preferably at least about 80%, more preferably at least about 85%, more preferably at least about 90% and even more preferably at least about 95% identical to nFeCD40₃₃₆, and/or an allelic variant of such a nucleic acid molecule. In one embodiment, a CD154 nucleic acid molecule of the present invention is at least
- 30 about 85%, preferably at least about 85%, more preferably at least about 90% and even more preferably at least about 95% identical to nCaCD154₃₉₀, nCaCD154₁₈₇₈,

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nCaCD154₇₈₀, and/or nCaCD154₆₃₃, and/or an allelic variant of such a nucleic acid molecule. In one embodiment, a CD154 nucleic acid molecule of the present invention is at least about 91%, and preferably about 95% identical to nFeCD154₈₈₅, nFeCD154₇₈₀, and/or nFeCD154₆₃₃, and/or an allelic variant of such a nucleic acid molecule. In one
5 embodiment, an IL-5 molecule of the present invention is at least about 90% and preferably at least about 95% identical to nCaIL-5₆₁₀, nCaIL-5₄₀₂, and/or nCaIL-5₃₄₅, and/or an allelic variant of such a nucleic acid molecule. In another embodiment, an IL-13 molecule of the present invention is at least about 65%, at least about 70%, preferably at least about 75%, more preferably at least about 80%, more preferably at least about
10 85%, more preferably at least about 90% and even more preferably at least about 95% identical to nCaIL-13₁₆₆, nCaIL-13₂₇₂, nCaIL-13₂₇₈, nCaIL-13₁₃₀₂, nCaIL-13₃₉₃, nCaIL-13₃₃₃, nCaIL-13₁₂₆₉, nCaIL-13₃₉₀, and/or nCaIL-13₃₃₀, and/or an allelic variant of such a nucleic acid molecule.

In another embodiment, an IL-4 nucleic acid molecule of the present invention
15 comprises a nucleic acid sequence that is at least about 90%, and preferably at least about 95% identical to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:19, and/or SEQ ID NO:21. The present invention also includes an IL-4 nucleic acid molecule comprising at least a portion of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:19, and/or SEQ ID NO:21, as well as allelic
20 variants of such IL-4 nucleic acid molecules, including nucleic acid molecules that have been modified to accommodate codon usage properties of the cells in which such nucleic acid molecules are to be expressed.

In another embodiment, a Flt-3 ligand nucleic acid molecule of the present invention comprises a nucleic acid sequence that is at least about 75%, preferably at least
25 about 80%, more preferably at least about 85%, more preferably at least about 90% and even more preferably at least about 95% identical to SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:36, and/or SEQ ID NO:37. The present invention
30 also includes a Flt-3 ligand- nucleic acid molecule comprising at least a portion of SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:22, SEQ ID

NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:36, and/or SEQ ID NO:37, as well as allelic variants of such Flt-3 ligand nucleic acid molecules, including nucleic acid molecules that have been modified to accommodate codon usage properties of the cells in which such nucleic acid molecules are to be expressed.

In one embodiment, a Flt-3 ligand nucleic acid molecule of the present invention comprises a nucleic acid sequence that is at least about 75%, more preferably at least about 80%, more preferably at least about 85%, more preferably at least about 90% and even more preferably at least about 95% identical to SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, and/or SEQ ID NO:50. The present invention also includes a Flt-3 ligand- nucleic acid molecule comprising at least a portion of SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, and/or SEQ ID NO:50, as well as allelic variants of such Flt-3 ligand nucleic acid molecules, including nucleic acid molecules that have been modified to accommodate codon usage properties of the cells in which such nucleic acid molecules are to be expressed.

In one embodiment, a CD40 nucleic acid molecule of the present invention comprises a nucleic acid sequence that is at least about 70%, at least about 75%, more preferably at least about 80%, more preferably at least about 85%, more preferably at least about 90% and even more preferably at least about 95% identical to SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, and/or SEQ ID NO:59. The present invention also includes a CD40 nucleic acid molecule comprising at least a portion of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, and/or SEQ ID NO:59, as well as allelic variants of such CD40 nucleic acid molecules, including nucleic acid molecules that have been modified to accommodate codon usage properties of the cells in which such nucleic acid molecules are to be expressed.

In one embodiment, a CD40 nucleic acid molecule of the present invention comprises a nucleic acid sequence that is at least about 70%, at least about 75%, more preferably at least about 80%, more preferably at least about 85%, more preferably at least about 90% and even more preferably at least about 95% identical to SEQ ID NO:60

and/or SEQ ID NO:62. The present invention also includes a CD40 nucleic acid molecule comprising at least a portion of SEQ ID NO:60 and/or SEQ ID NO:62, as well as allelic variants of such CD40 nucleic acid molecules, including nucleic acid molecules that have been modified to accommodate codon usage properties of the cells in which such nucleic acid molecules are to be expressed.

In one embodiment, a CD154 nucleic acid molecule of the present invention comprises a nucleic acid sequence that is at least about 85%, preferably at least about 85%, more preferably at least about 90% and even more preferably at least about 95% identical to SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, and/or SEQ ID NO:71. The present invention also includes a CD154 nucleic acid molecule comprising at least a portion of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, and/or SEQ ID NO:71, as well as allelic variants of such CD154 nucleic acid molecules, including nucleic acid molecules that have been modified to accommodate codon usage properties of the cells in which such nucleic acid molecules are to be expressed.

In one embodiment, a CD154 nucleic acid molecule of the present invention comprises a nucleic acid sequence that is at least about 91%, and preferably about 95% identical to SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, and/or SEQ ID NO:79. The present invention also includes a CD154 nucleic acid molecule comprising at least a portion of SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, and/or SEQ ID NO:79, as well as allelic variants of such CD154 nucleic acid molecules, including nucleic acid molecules that have been modified to accommodate codon usage properties of the cells in which such nucleic acid molecules are to be expressed.

In one embodiment, an IL-5 nucleic acid molecule of the present invention comprises a nucleic acid sequence that is at least about 90% and preferably at least about 95% identical to SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, and/or SEQ ID NO:87. The present invention also includes an IL-5 nucleic acid molecule comprising at least a portion of SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, and/or SEQ ID NO:87, as well as allelic variants of such IL-5 nucleic acid molecules, including nucleic acid molecules that have

been modified to accommodate codon usage properties of the cells in which such nucleic acid molecules are to be expressed.

In one embodiment, an IL-13 nucleic acid molecule of the present invention comprises a nucleic acid sequence that is at least about 65%, at least about 70%, preferably at least about 75%, more preferably at least about 80%, more preferably at least about 85%, more preferably at least about 90% and even more preferably at least about 95% identical to SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, and/or SEQ ID NO:106. The present invention also includes an IL-13 nucleic acid molecule comprising at least a portion of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, and/or SEQ ID NO:106, as well as allelic variants of such IL-13 nucleic acid molecules, including nucleic acid molecules that have been modified to accommodate codon usage properties of the cells in which such nucleic acid molecules are to be expressed.

In one embodiment, an IFN α nucleic acid molecule of the present invention is identical to SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:116, and/or SEQ ID NO:118.

In another embodiment, a GM-CSF nucleic acid molecule of the present invention is identical to SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, and/or SEQ ID NO:126.

Knowing the nucleic acid sequences of certain immunoregulatory nucleic acid molecules of the present invention allows one skilled in the art to, for example, (a) make copies of those nucleic acid molecules, (b) obtain nucleic acid molecules including at least a portion of such nucleic acid molecules (e.g., nucleic acid molecules including full-length genes, full-length coding regions, regulatory control sequences, truncated coding regions), and/or (c) obtain other immunoregulatory nucleic acid molecules. Such nucleic acid molecules can be obtained in a variety of ways including screening appropriate expression libraries with antibodies of the present invention; traditional

cloning techniques using oligonucleotide probes of the present invention to screen appropriate libraries; and PCR amplification of appropriate libraries or DNA using oligonucleotide primers of the present invention. Preferred libraries to screen or from which to amplify nucleic acid molecules include mammalian cDNA libraries as well as
5 genomic DNA libraries. Similarly, preferred DNA sources from which to amplify nucleic acid molecules include mammalian cDNA and genomic DNA. Techniques to clone and amplify genes are disclosed, for example, in Sambrook et al., *ibid.*

The present invention also includes nucleic acid molecules that are oligonucleotides capable of hybridizing, under stringent hybridization conditions, with
10 complementary regions of other, preferably longer, nucleic acid molecules of the present invention such as those comprising canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF nucleic acid molecules. Oligonucleotides of the present invention can be RNA, DNA, or derivatives of either. The minimum size
15 of such oligonucleotides is the size required for formation of a stable hybrid between an oligonucleotide and a complementary sequence on a nucleic acid molecule of the present invention. A preferred oligonucleotide of the present invention has a maximum size of about 100 nucleotides. The present invention includes oligonucleotides that can be used as, for example, probes to identify nucleic acid molecules, primers to produce nucleic
20 acid molecules, or therapeutic reagents to inhibit canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF protein production or activity (e.g., as antisense-, triplex formation-, ribozyme- and/or RNA drug-based reagents). The present invention also includes the use of such oligonucleotides to protect animals from
25 disease using one or more of such technologies. Appropriate oligonucleotide-containing therapeutic compositions can be administered to an animal using techniques known to those skilled in the art.

One embodiment of the present invention includes a recombinant vector, which includes at least one isolated nucleic acid molecule of the present invention, inserted into
30 any vector capable of delivering the nucleic acid molecule into a host cell. Such a vector contains heterologous nucleic acid sequences, that is nucleic acid sequences that are not

naturally found adjacent to nucleic acid molecules of the present invention and that preferably are derived from a species other than the species from which the nucleic acid molecule(s) are derived. The vector can be either RNA or DNA, either prokaryotic or eukaryotic, and typically is a virus or a plasmid. Recombinant vectors can be used in the cloning, sequencing, and/or otherwise manipulating immunoregulatory nucleic acid molecules of the present invention.

One type of recombinant vector, referred to herein as a recombinant molecule, comprises a nucleic acid molecule of the present invention operatively linked to an expression vector. The phrase operatively linked refers to insertion of a nucleic acid molecule into an expression vector in a manner such that the molecule is able to be expressed when transformed into a host cell. As used herein, an expression vector is a DNA or RNA vector that is capable of transforming a host cell and of effecting expression of a specified nucleic acid molecule. Preferably, the expression vector is also capable of replicating within the host cell. Expression vectors can be either prokaryotic or eukaryotic, and are typically viruses or plasmids. Expression vectors of the present invention include any vectors that function (i.e., direct gene expression) in recombinant cells of the present invention, including in bacterial, fungal, parasite, insect, other animal, and plant cells. Preferred expression vectors of the present invention can direct gene expression in bacterial, yeast, insect and mammalian cells, and more preferably in the cell types disclosed herein, more preferably *in vivo*.

In particular, expression vectors of the present invention contain regulatory sequences such as transcription control sequences, translation control sequences, origins of replication, and other regulatory sequences that are compatible with the recombinant cell and that control the expression of nucleic acid molecules of the present invention. In particular, recombinant molecules of the present invention include transcription control sequences. Transcription control sequences are sequences which control the initiation, elongation, and termination of transcription. Particularly important transcription control sequences are those which control transcription initiation, such as promoter, enhancer, operator and repressor sequences. Suitable transcription control sequences include any transcription control sequence that can function in at least one of the recombinant cells of the present invention. A variety of such transcription control

sequences are known to those skilled in the art. Preferred transcription control sequences include those which function in bacterial, yeast, helminth and/or other endoparasite, insect and mammalian cells, such as, but not limited to, *tac*, *lac*, *trp*, *trc*, oxy-pro, omp/lpp, rmb, bacteriophage lambda (such as lambda p_L and lambda p_R and fusions that include such promoters), bacteriophage T7, T7*lac*, bacteriophage T3, bacteriophage SP6, bacteriophage SP01, metallothionein, alpha-mating factor, *Pichia* alcohol oxidase, alphavirus subgenomic promoter, antibiotic resistance gene, baculovirus, *Heliothis zea* insect virus, vaccinia virus, herpesvirus, raccoon poxvirus, other poxvirus, adenovirus, cytomegalovirus (such as immediate early promoter), simian virus 40, retrovirus, actin, retroviral long terminal repeat, Rous sarcoma virus, heat shock, phosphate and nitrate transcription control sequences as well as other sequences capable of controlling gene expression in prokaryotic or eukaryotic cells. Additional suitable transcription control sequences include tissue-specific promoters and enhancers as well as lymphokine-inducible promoters (e.g., promoters inducible by interferons or interleukins). Transcription control sequences of the present invention can also include naturally occurring transcription control sequences naturally associated with mammals, such as dog, cat, horse or human transcription control sequences.

Suitable and preferred nucleic acid molecules to include in recombinant vectors of the present invention are as disclosed herein. Preferred nucleic acid molecules to include in recombinant vectors, and particularly in recombinant molecules, include nCaIL-4₅₄₉, nCaIL-4₃₉₆, nCaIL-4₃₂₄, nCaFlt3L₁₀₁₃, nCaFlt3L₈₈₂, nCaFlt3L₈₀₄, nCaFlt3L₈₂₈, nCaFlt3L₉₈₅, nCaFlt3L₁₀₁₉, nCaFlt3L₉₃, nCaFlt3L₇₅₀, nFeFlt3L₃₉₅, nFeFlt3L₇₉₃, nFeFlt3L₉₄₂, nFeFlt3L₈₇₃, nFeFlt3L₇₉₅, nCaCD40₃₂₁, nCaCD40₁₄₂₅, nCaCD40₈₂₂, nCaCD40₇₆₅, nFeCD40₃₃₆, nCaCD154₃₉₀, nCaCD154₁₈₇₈, nCaCD154₇₈₀, nCaCD154₆₃₃, nFeCD154₈₈₅, nFeCD154₇₈₀, nFeCD154₆₃₃, nCaIL-5₆₁₀, nCaIL-5₄₀₂, nCaIL-5₃₄₅, nCaIL-13₁₆₆, nCaIL-13₂₇₂, nCaIL-13₂₇₈, nCaIL-13₁₃₀₂, nCaIL-13₃₉₃, nCaIL-13₃₃₃, nCaIL-13₁₂₆₉, nCaIL-13₃₉₀, nCaIL-13₃₃₀, nFeIFN α _{567a}, nFeIFN α _{567b}, nFeIFN α _{498a}, nFeIFN α _{498b}, nFeGMCSF₄₄₄, nFeGMCSF₄₃₂, and/or nFeGMCSF₃₈₁.

Recombinant molecules of the present invention may also (a) contain secretory signals (i.e., signal segment nucleic acid sequences) to enable an expressed parasitic helminth protein of the present invention to be secreted from the cell that produces the

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protein and/or (b) contain fusion sequences which lead to the expression of nucleic acid molecules of the present invention as fusion proteins. Examples of suitable signal segments include any signal segment capable of directing the secretion of a protein of the present invention. Preferred signal segments include, but are not limited to, tissue plasminogen activator (t-PA), interferon, interleukin, growth hormone, histocompatibility and viral envelope glycoprotein signal segments. Suitable fusion segments encoded by fusion segment nucleic acids are disclosed herein. In addition, a nucleic acid molecule of the present invention can be joined to a fusion segment that directs the encoded protein to the proteosome, such as a ubiquitin fusion segment.

10 Eukaryotic recombinant molecules may also include intervening and/or untranslated sequences surrounding and/or within the nucleic acid sequences of nucleic acid molecules of the present invention.

Another embodiment of the present invention includes a recombinant cell comprising a host cell transformed with one or more recombinant molecules of the present invention. Transformation of a nucleic acid molecule into a cell can be accomplished by any method by which a nucleic acid molecule can be inserted into the cell. Transformation techniques include, but are not limited to, transfection, electroporation, microinjection, lipofection, adsorption, and protoplast fusion. A recombinant cell may remain unicellular or may grow into a tissue, organ or a multicellular organism. Transformed nucleic acid molecules of the present invention can remain extrachromosomal or can integrate into one or more sites within a chromosome of the transformed (i.e., recombinant) cell in such a manner that their ability to be expressed is retained. Preferred nucleic acid molecules with which to transform a cell include immunoregulatory nucleic acid molecules of the present invention disclosed herein. Particularly preferred nucleic acid molecules with which to transform a cell include nCaIL-4₅₄₉, nCaIL-4₃₉₆, nCaIL-4₃₂₄, nCaFlt3L₁₀₁₃, nCaFlt3L₈₈₂, nCaFlt3L₈₀₄, nCaFlt3L₈₂₈, nCaFlt3L₉₈₅, nCaFlt3L₁₀₁₉, nCaFlt3L₉₃, nCaFlt3L₇₅₀, nFeFlt3L₃₉₅, nFeFlt3L₇₉₃, nFeFlt3L₉₄₂, nFeFlt3L₈₇₃, nFeFlt3L₇₉₅, nCaCD40₃₂₁, nCaCD40₁₄₂₅, nCaCD40₈₂₂, nCaCD40₇₆₅, nFeCD40₃₃₆, nCaCD154₃₉₀, nCaCD154₁₈₇₈, nCaCD154₇₈₀, nCaCD154₆₃₃, nFeCD154₈₈₅, nFeCD154₇₈₀, nFeCD154₆₃₃, nCaIL-5₆₁₀, nCaIL-5₄₀₂, nCaIL-5₃₄₅, nCaIL-13₁₆₆, nCaIL-13₂₇₂, nCaIL-13₂₇₈, nCaIL-13₁₃₀₂, nCaIL-

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13₃₉₃, nCaIL-13₃₃₃, nCaIL-13₁₂₆₉, nCaIL-13₃₉₀, nCaIL-13₃₃₀, nFeIFN α _{567a}, nFeIFN α _{567b},
nFeIFN α _{498a}, nFeIFN α _{498b}, nFeGMCSF₄₄₄, nFeGMCSF₄₃₂, and/or nFeGMCSF₃₈₁.

Suitable host cells to transform include any cell that can be transformed with a nucleic acid molecule of the present invention. Host cells can be either untransformed
5 cells or cells that are already transformed with at least one nucleic acid molecule (e.g., nucleic acid molecules encoding one or more proteins of the present invention and/or other proteins useful in the production of multivalent vaccines). Host cells of the present invention either can be endogenously (i.e., naturally) capable of producing immunoregulatory proteins of the present invention or can be capable of producing such
10 proteins after being transformed with at least one nucleic acid molecule of the present invention. Host cells of the present invention can be any cell capable of producing at least one protein of the present invention, and include bacterial, fungal (including yeast), parasite (including helminth, protozoa and ectoparasite), other insect, other animal and plant cells. Preferred host cells include bacterial, mycobacterial, yeast, helminth, insect
15 and mammalian cells. More preferred host cells include *Salmonella*, *Escherichia*, *Bacillus*, *Listeria*, *Saccharomyces*, *Spodoptera*, *Mycobacteria*, *Trichoplusia*, BHK (baby hamster kidney) cells, MDCK cells (Madin-Darby canine kidney cell line), CRFK cells (Crandell feline kidney cell line), CV-1 cells (African monkey kidney cell line used, for example, to culture raccoon poxvirus), COS (e.g., COS-7) cells, chinese hamster ovary
20 (CHO) cells, Ltk cells and Vero cells. Particularly preferred host cells are *Escherichia coli*, including *E. coli* K-12 derivatives; *Salmonella typhi*; *Salmonella typhimurium*, including attenuated strains such as UK-1₀₃₉₈₇ and SR-11₀₄₀₇₂; *Spodoptera frugiperda*; *Trichoplusia ni*; BHK cells; MDCK cells; CRFK cells; CV-1 cells; COS cells; Vero cells; and non-tumorigenic mouse myoblast G8 cells (e.g., ATCC CRL
25 1246). Additional appropriate mammalian cell hosts include other kidney cell lines, other fibroblast cell lines (e.g., human, murine or chicken embryo fibroblast cell lines), myeloma cell lines, Chinese hamster ovary cells, mouse NIH/3T3 cells, LMTK³¹ cells and/or HeLa cells. In one embodiment, the proteins may be expressed as heterologous proteins in myeloma cell lines employing immunoglobulin promoters.

30 A recombinant cell is preferably produced by transforming a host cell with one or more recombinant molecules, each comprising one or more nucleic acid molecules of

the present invention operatively linked to an expression vector containing one or more transcription control sequences, examples of which are disclosed herein.

A recombinant cell of the present invention includes any cell transformed with at least one of any nucleic acid molecule of the present invention. Suitable and preferred
5 nucleic acid molecules as well as suitable and preferred recombinant molecules with which to transfer cells are disclosed herein.

Recombinant cells of the present invention can also be co-transformed with one or more recombinant molecules including any of canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine
10 interleukin-13, feline interferon alpha, or feline GM-CSF nucleic acid molecule encoding one or more proteins of the present invention and/or one or more other nucleic acid molecules encoding other therapeutic compounds, as disclosed herein (e.g., to produce multivalent vaccines).

Recombinant DNA technologies can be used to improve expression of
15 transformed nucleic acid molecules by manipulating, for example, the number of copies of the nucleic acid molecules within a host cell, the efficiency with which those nucleic acid molecules are transcribed, the efficiency with which the resultant transcripts are translated, and the efficiency of post-translational modifications. Recombinant techniques useful for increasing the expression of nucleic acid molecules of the present
20 invention include, but are not limited to, operatively linking nucleic acid molecules to high-copy number plasmids, integration of the nucleic acid molecules into one or more host cell chromosomes, addition of vector stability sequences to plasmids, substitutions or modifications of transcription control signals (e.g., promoters, operators, enhancers), substitutions or modifications of translational control signals (e.g., ribosome binding
25 sites, Shine-Dalgarno sequences), modification of nucleic acid molecules of the present invention to correspond to the codon usage of the host cell, deletion of sequences that destabilize transcripts, and use of control signals that temporally separate recombinant cell growth from recombinant enzyme production during fermentation. The activity of an expressed recombinant protein of the present invention may be improved by
30 fragmenting, modifying, or derivatizing nucleic acid molecules encoding such a protein.

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Isolated immunoregulatory proteins of the present invention can be produced in a variety of ways, including production and/or recovery of natural proteins, production and/or recovery of recombinant proteins, and/or chemical synthesis of the proteins. In one embodiment, an isolated protein of the present invention is produced by culturing a cell capable of expressing the protein under conditions effective to produce the protein, and recovering the protein. A preferred cell to culture is a recombinant cell of the present invention. Effective culture conditions include, but are not limited to, effective media, bioreactor, temperature, pH and oxygen conditions that permit protein production. An effective medium refers to any medium in which a cell is cultured to produce an immunoregulatory protein of the present invention. Such medium typically comprises an aqueous medium having assimilable carbon, nitrogen and phosphate sources, and appropriate salts, minerals, metals and other nutrients, such as vitamins. Cells of the present invention can be cultured in conventional fermentation bioreactors, shake flasks, test tubes, microtiter dishes, and petri plates. Culturing can be carried out at a temperature, pH and oxygen content appropriate for a recombinant cell. Such culturing conditions are within the expertise of one of ordinary skill in the art.

Depending on the vector and host system used for production, resultant proteins of the present invention may either remain within the recombinant cell; be secreted into the fermentation medium; be secreted into a space between two cellular membranes, such as the periplasmic space in *E. coli*; or be retained on the outer surface of a cell or viral membrane.

The phrase "recovering the protein", as well as similar phrases, refers to collecting the whole fermentation medium containing the protein and need not imply additional steps of separation or purification. Proteins of the present invention can be purified using a variety of standard protein purification techniques, such as, but not limited to, affinity chromatography, ion exchange chromatography, filtration, electrophoresis, hydrophobic interaction chromatography, gel filtration chromatography, reverse phase chromatography, concanavalin A chromatography, chromatofocusing and/or differential solubilization. Proteins of the present invention are preferably retrieved in "substantially pure" form. As used herein, "substantially pure" refers to a purity that allows for the effective use of the protein as a therapeutic composition or

diagnostic. A therapeutic composition for animals, for example, should exhibit no substantial toxicity and preferably should be capable of stimulating the production of antibodies in a treated animal.

The present invention also includes isolated (i.e., removed from their natural milieu) antibodies that selectively bind to an immunoregulatory protein of the present invention and/or a mimetope thereof (e.g., anti-IL-4 antibodies, anti-Flt-3 ligand antibodies, anti-CD40 antibodies, anti-CD154 antibodies, anti-IL-5 antibodies, anti-IL-13 antibodies, anti-IFN α antibodies, and/or anti-GM-CSF antibodies). As used herein, the term "selectively binds to" an immunoregulatory protein of the present invention, refers to the ability of antibodies of the present invention to preferentially bind to specified proteins and/or mimetopes thereof of the present invention. Binding can be measured using a variety of methods standard in the art including enzyme immunoassays (e.g., ELISA), immunoblot assays, etc.; see, for example, Sambrook et al., *ibid.*, and Harlow, et al., 1988, *Antibodies, a Laboratory Manual*, Cold Spring Harbor Labs Press; Harlow et al., *ibid.* An anti-IL-4 antibody of the present invention preferably selectively binds to an IL-4 protein in such a way as to inhibit the function of that protein. An anti-Flt-3 ligand antibody of the present invention preferably selectively binds to a Flt-3 ligand- protein in such a way as to inhibit the function of that protein. An anti-CD40 antibody of the present invention preferably selectively binds to a CD40 protein in such a way as to inhibit the function of that protein. An anti-CD154 antibody of the present invention preferably selectively binds to a CD154 protein in such a way as to inhibit the function of that protein. An anti-IL-5 antibody of the present invention preferably selectively binds to an IL-5 protein in such a way as to inhibit the function of that protein. An anti-IL-13 antibody of the present invention preferably selectively binds to an IL-13 protein in such a way as to inhibit the function of that protein. An anti-IFN α antibody of the present invention preferably selectively binds to an IFN α protein in such a way as to inhibit the function of that protein. An anti-GM-CSF antibody of the present invention preferably selectively binds to a GM-CSF protein in such a way as to inhibit the function of that protein.

Isolated antibodies of the present invention can include antibodies in serum, or antibodies that have been purified to varying degrees. Antibodies of the present

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invention can be polyclonal or monoclonal, or can be functional equivalents such as antibody fragments and/or genetically-engineered antibodies, including single chain antibodies or chimeric antibodies that can bind to one or more epitopes.

A preferred method to produce antibodies of the present invention includes (a) administering to an animal an effective amount of a protein, peptide and/or mimotope thereof of the present invention to produce the antibodies and (b) recovering the antibodies. In another method, antibodies of the present invention are produced recombinantly using techniques as heretofore disclosed to produce any of the immunoregulatory proteins of the present invention. Antibodies raised against defined proteins or mimetopes can be advantageous because such antibodies are not substantially contaminated with antibodies against other substances that might otherwise cause interference in a diagnostic assay or side effects if used in a therapeutic composition.

Antibodies of the present invention have a variety of potential uses that are within the scope of the present invention. For example, such antibodies can be used (a) as reagents in assays to detect an immunoregulatory protein of the present invention, (b) as reagents in assays to modulate cellular activity through an immunoregulatory protein of the present invention (e.g., mimicking ligand binding to a canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, or feline GM-CSF protein, as appropriate), and/or (c) as tools to screen expression libraries and/or to recover desired proteins of the present invention from a mixture of proteins and other contaminants. Furthermore, antibodies of the present invention can be used to target compounds (e.g., nucleic acid molecules, drugs or proteins) to antigen presenting cells. Targeting can be accomplished by conjugating (i.e., stably joining) such antibodies to the compounds using techniques known to those skilled in the art. Suitable compounds are known to those skilled in the art.

One embodiment of the present invention is a therapeutic composition that, when administered to an animal in an effective manner, is capable of regulating an immune response in an animal. Therapeutic compositions of the present invention can include at least one of the following therapeutic compounds: an isolated IL-4, Flt-3 ligand, CD40, CD154, IL-5, IL-13, IFN α , and/or GM-CSF protein of the present invention and/or a

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mimotope thereof; an isolated IL-4, Flt-3 ligand, CD40, CD154, IL-5, IL-13, IFN α , and/or GM-CSF nucleic acid molecule of the present invention; an isolated antibody that selectively binds to an IL-4, Flt-3 ligand, CD40, CD154, IL-5, IL-13, IFN α , and/or GM-CSF protein of the present invention; an inhibitor of canine IL-4, Flt-3 ligand, CD40, CD154, IL-5, IL-13, IFN α , and/or GM-CSF function identified by its ability to bind to an IL-4, Flt-3 ligand, CD40, CD154, IL-5, IL-13, IFN α , and/or GM-CSF protein, respectively, of the present invention; such an inhibitor can inhibit binding of the respective immunoregulatory protein with its respective receptor, or inhibit the activity of the respective protein. Methods to perform such assays to measure binding and/or activity of an immunoregulatory protein of the present invention are known to those of skill in the art, and are described, for example, in Janeway et al., *ibid*. As used herein, a therapeutic compound refers to a compound that, when administered to an animal in an effective manner, is able to treat, ameliorate, and/or prevent a disease. Examples of proteins, nucleic acid molecules, antibodies and/or inhibitors of the present invention are disclosed herein.

The present invention also includes a therapeutic composition comprising at least one IL-4-, Flt-3 ligand-, CD40-, CD154-, IL-5-, IL-13-, IFN α -, and/or GM-CSF-based compound of the present invention in combination with at least one additional therapeutic compound. Examples of such compounds are disclosed herein.

Therapeutic compositions of the present invention can be administered to any animal susceptible to such therapy, preferably to mammals, and more preferably to dogs, cats, humans, ferrets, horses, cattle, sheep and/or other pets, economic food animals and/or zoo animals. Preferred animals include dogs, cats, horses and/or humans.

A therapeutic composition of the present invention is administered to an animal in an effective manner such that the composition is capable of regulating an immune response in that animal. Therapeutic compositions of the present invention can be administered to animals prior to onset of a disease (i.e., as a preventative vaccine) and/or can be administered to animals after onset of a disease in order to treat the disease (i.e., as a therapeutic vaccine). Preferred diseases to prevent and/or treat include autoimmune diseases, allergic reactions, infectious diseases, tumor development, inflammatory diseases and/or graft rejection. In one embodiment, a therapeutic

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composition of the present invention is administered with an antigen to enhance an immune response against that antigen.

Therapeutic compositions of the present invention can be formulated in an excipient that the animal to be treated can tolerate. Examples of such excipients include water, saline, Ringer's solution, dextrose solution, Hank's solution, and/or other aqueous physiologically balanced salt solutions. Nonaqueous vehicles, such as fixed oils, sesame oil, ethyl oleate, or triglycerides may also be used. Other useful formulations include suspensions containing viscosity enhancing agents, such as sodium carboxymethylcellulose, sorbitol, or dextran. Excipients can also contain minor amounts of additives, such as substances that enhance isotonicity and chemical stability. Examples of buffers include phosphate buffer, bicarbonate buffer and/or Tris buffer, while examples of preservatives include thimerosal, o-cresol, formalin and/or benzyl alcohol. Standard formulations can either be liquid injectables or solids which can be taken up in a suitable liquid as a suspension or solution for injection. Thus, in a non-liquid formulation, the excipient can comprise dextrose, human serum albumin, preservatives, etc., to which sterile water or saline can be added prior to administration.

In one embodiment of the present invention, a therapeutic composition can include an adjuvant. Adjuvants are agents that are capable of enhancing the immune response of an animal to a specific antigen. Suitable adjuvants include, but are not limited to, cytokines, chemokines, and/or compounds that induce the production of cytokines and/or chemokines (e.g., granulocyte macrophage colony stimulating factor (GM-CSF), granulocyte colony stimulating factor (G-CSF), macrophage colony stimulating factor (M-CSF), colony stimulating factor (CSF), erythropoietin (EPO), interleukin 2 (IL-2), interleukin-3 (IL-3), interleukin 5 (IL-5), interleukin 6 (IL-6), interleukin 7 (IL-7), interleukin 8 (IL-8), interleukin 10 (IL-10), interleukin 12 (IL-12), interferon gamma, interferon gamma inducing factor I (IGIF), transforming growth factor beta, RANTES (regulated upon activation, normal T cell expressed and presumably secreted), macrophage inflammatory proteins (e.g., MIP-1 alpha and MIP-1 beta), and Leishmania elongation initiating factor (LEIF)); bacterial components (e.g., endotoxins, in particular superantigens, exotoxins and cell wall components); aluminum-based salts; calcium-based salts; silica; polynucleotides; toxoids; serum

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proteins, viral coat proteins; block copolymer adjuvants (e.g., Hunter's Titermax™ adjuvant (Vaxcel™, Inc. Norcross, GA), Ribi adjuvants (Ribi ImmunoChem Research, Inc., Hamilton, MT); and saponins and their derivatives (e.g., Quil A (Superfos Biosector A/S, Denmark). Protein adjuvants of the present invention can be delivered in the form of the protein themselves or of nucleic acid molecules encoding such proteins using the methods described herein.

In one embodiment of the present invention, a therapeutic composition can include a carrier. Carriers include compounds that increase the half-life of a therapeutic composition in the treated animal. Suitable carriers include, but are not limited to, polymeric controlled release vehicles, biodegradable implants, liposomes, bacteria, viruses, other cells, oils, esters, and glycols.

One embodiment of the present invention is a controlled release formulation that is capable of slowly releasing a composition of the present invention into an animal. As used herein, a controlled release formulation comprises a composition of the present invention in a controlled release vehicle. Suitable controlled release vehicles include, but are not limited to, biocompatible polymers, other polymeric matrices, capsules, microcapsules, microparticles, bolus preparations, osmotic pumps, diffusion devices, liposomes, lipospheres, and transdermal delivery systems. Other controlled release formulations of the present invention include liquids that, upon administration to an animal, form a solid or a gel *in situ*. Preferred controlled release formulations are biodegradable (i.e., bioerodible).

A preferred controlled release formulation of the present invention is capable of releasing a composition of the present invention into the blood of the treated animal at a constant rate sufficient to attain therapeutic dose levels of the composition to regulate an immune response in an animal. The therapeutic composition is preferably released over a period of time ranging from about 1 to about 12 months. A controlled release formulation of the present invention is capable of effecting a treatment preferably for at least about 1 month, more preferably for at least about 3 months, even more preferably for at least about 6 months, even more preferably for at least about 9 months, and even more preferably for at least about 12 months.

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Therapeutic compositions of the present invention can be administered to animals prior to and/or after onset of disease. Acceptable protocols to administer therapeutic compositions in an effective manner include individual dose size, number of doses, frequency of dose administration, and/or mode of administration. Determination of such protocols can be accomplished by those skilled in the art. A suitable single dose is a dose that is capable of regulating the immune response in an animal when administered one or more times over a suitable time period. For example, a preferred single dose of a protein, mimotope or antibody therapeutic composition is from about 1 microgram (μg) to about 10 milligrams (mg) of the therapeutic composition per kilogram body weight of the animal. Booster vaccinations can be administered from about 2 weeks to several years after the original administration. Booster administrations preferably are administered when the immune response of the animal becomes insufficient to protect the animal from disease. A preferred administration schedule is one in which from about 10 μg to about 1 mg of the therapeutic composition per kg body weight of the animal is administered from about one to about two times over a time period of from about 2 weeks to about 12 months. Modes of administration can include, but are not limited to, subcutaneous, intradermal, intravenous, intranasal, intraocular, oral, transdermal and/or intramuscular routes.

According to one embodiment, a nucleic acid molecule of the present invention can be administered to an animal in a fashion to enable expression of that nucleic acid molecule into a therapeutic protein or therapeutic RNA (e.g., antisense RNA, ribozyme, triple helix forms or RNA drug) in the animal. Nucleic acid molecules can be delivered to an animal in a variety of methods including, but not limited to, (a) administering a naked (i.e., not packaged in a viral coat or cellular membrane) nucleic acid as a genetic vaccine (e.g., as naked DNA or RNA molecules, such as is taught, for example in Wolff et al., 1990, *Science* 247, 1465-1468) or (b) administering a nucleic acid molecule packaged as a recombinant virus vaccine or as a recombinant cell vaccine (i.e., the nucleic acid molecule is delivered by a viral or cellular vehicle).

A genetic (i.e., naked nucleic acid) vaccine of the present invention includes a nucleic acid molecule of the present invention and preferably includes a recombinant molecule of the present invention that preferably is replication, or otherwise

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amplification, competent. A genetic vaccine of the present invention can comprise one or more nucleic acid molecules of the present invention in the form of, for example, a dicistronic recombinant molecule. Preferred genetic vaccines include at least a portion of a viral genome (i.e., a viral vector). Preferred viral vectors include those based on
5 alphaviruses, poxviruses, adenoviruses, herpesviruses, picornaviruses, and/or retroviruses, with those based on alphaviruses (such as Sindbis or Semliki forest virus), species-specific herpesviruses and/or poxviruses being particularly preferred. Any suitable transcription control sequence can be used, including those disclosed as suitable for protein production. Particularly preferred transcription control sequences include
10 cytomegalovirus immediate early (preferably in conjunction with Intron-A), Rous sarcoma virus long terminal repeat, and tissue-specific transcription control sequences, as well as transcription control sequences endogenous to viral vectors if viral vectors are used. The incorporation of a "strong" polyadenylation signal is also preferred.

Genetic vaccines of the present invention can be administered in a variety of
15 ways, with intramuscular, subcutaneous, intradermal, transdermal, intranasal and/or oral routes of administration being preferred. A preferred single dose of a genetic vaccine ranges from about 1 nanogram (ng) to about 600 μ g, depending on the route of administration and/or method of delivery, as can be determined by those skilled in the art. Suitable delivery methods include, for example, by injection, as drops, aerosolized
20 and/or topically. Genetic vaccines of the present invention can be contained in an aqueous excipient (e.g., phosphate buffered saline) alone or in a carrier (e.g., lipid-based vehicles).

A recombinant virus vaccine of the present invention includes a recombinant molecule of the present invention that is packaged in a viral coat and that can be
25 expressed in an animal after administration. Preferably, the recombinant molecule is packaging- or replication-deficient and/or encodes an attenuated virus. A number of recombinant viruses can be used, including, but not limited to, those based on alphaviruses, poxviruses, adenoviruses, herpesviruses, picornaviruses, and/or retroviruses. Preferred recombinant virus vaccines are those based on alphaviruses (such
30 as Sindbis virus), raccoon poxviruses, species-specific herpesviruses and/or species-specific poxviruses. An example of methods to produce and use alphavirus

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recombinant virus vaccines are disclosed in U.S. Patent Number 5,766,602 by Xiong et al., issued June 16, 1998.

When administered to an animal, a recombinant virus vaccine of the present invention infects cells within the immunized animal and directs the production of a therapeutic protein or RNA nucleic acid molecule that is capable of protecting the animal from disease caused by a parasitic helminth as disclosed herein. For example, a recombinant virus vaccine comprising an immunoregulatory nucleic acid molecule of the present invention is administered according to a protocol that results in the regulation of an immune response in an animal. A preferred single dose of a recombinant virus vaccine of the present invention is from about 1×10^4 to about 1×10^8 virus plaque forming units (pfu) per kilogram body weight of the animal. Administration protocols are similar to those described herein for protein-based vaccines, with subcutaneous, intramuscular, intranasal, intraocular and/or oral administration routes being preferred.

A recombinant cell vaccine of the present invention includes recombinant cells of the present invention that express at least one protein of the present invention. Preferred recombinant cells for this embodiment include *Salmonella*, *E. coli*, *Listeria*, *Mycobacterium*, *S. frugiperda*, yeast, (including *Saccharomyces cerevisiae* and *Pichia pastoris*), BHK, CV-1, myoblast G8, COS (e.g., COS-7), Vero, MDCK and CRFK recombinant cells. Recombinant cell vaccines of the present invention can be administered in a variety of ways but have the advantage that they can be administered orally, preferably at doses ranging from about 10^8 to about 10^{12} cells per kilogram body weight. Administration protocols are similar to those described herein for protein-based vaccines. Recombinant cell vaccines can comprise whole cells, cells stripped of cell walls or cell lysates.

The efficacy of a therapeutic composition of the present invention to regulate the immune response in an animal can be tested in a variety of ways including, but not limited to, detection of cellular immunity within the treated animal, determining lymphocyte or dendritic cell activity, detection of immunoglobulin levels, determining hematopoietic stem cell or hematopoietic early progenitor cell development, determining dendritic cell development or challenge of the treated animal with an infectious agent to determine whether the treated animal is resistant to disease. In one embodiment,

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therapeutic compositions can be tested in animal models such as mice. Such techniques are known to those skilled in the art.

One embodiment of the present invention is an inhibitory compound. Preferably, such an inhibitory compound is derived from an IL-4, Flt-3 ligand, CD40, CD154, IL-5, IL-13, IFN α , and/or GM-CSF protein of the present invention. Examples of inhibitory compounds include an antibody of the present invention, that is administered to an animal in an effective manner (i.e., is administered in an amount so as to be present in the animal at a titer that is sufficient, upon interaction of that antibody with a native IL-4, Flt-3 ligand, CD40, CD154, IL-5, IL-13, IFN α , and/or GM-CSF protein, to decrease the activity of such proteins in an animal, at least temporarily). Oligonucleotide nucleic acid molecules of the present invention can also be administered in an effective manner, thereby reducing expression of either an IL-4, Flt-3 ligand, CD40, CD154, IL-5, IL-13, IFN α , and/or GM-CSF protein, in order to interfere with the protein activity targeted in accordance with the present invention. Peptides of an IL-4, Flt-3 ligand, CD40, CD154, IL-5, IL-13, IFN α , and/or GM-CSF protein of the present invention can also be administered in an effective manner, thereby reducing binding of IL-4, Flt-3 ligand, CD40, CD154, IL-5, IL-13, IFN α , and/or GM-CSF proteins to the appropriate receptor, in order to interfere with the protein activity targeted in accordance with the present invention. An inhibitory compound of an IL-4, Flt-3 ligand, CD40, CD154, IL-5, IL-13, IFN α , and/or GM-CSF function can be identified using IL-4, Flt-3 ligand, CD40, CD154, IL-5, IL-13, IFN α , and/or GM-CSF proteins of the present invention, respectively.

One embodiment of the present invention is a method to identify a compound capable of inhibiting IL-4 function. Such a method includes the steps of: (a) contacting (e.g., combining, mixing) an isolated IL-4 protein of the present invention, with a putative inhibitory compound under conditions in which, in the absence of the compound, the IL-4 protein binds to IL-4 receptor or stimulates T cells in a T cell proliferation assay, and (b) determining if the putative inhibitory compound inhibits the binding of IL-4 protein to IL-4 receptor or the stimulation of T cells in a T cell proliferation assay. Another embodiment of the present invention is a method to identify a compound capable of inhibiting Flt-3 ligand function. Such a method includes the

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steps of: (a) contacting an isolated Flt-3 ligand protein of the present invention, with a putative inhibitory compound under conditions in which, in the absence of the compound, the Flt-3 ligand protein binds to Flt-3 receptor or stimulates dendritic precursor cells in a proliferation assay, and (b) determining if the putative inhibitory compound inhibits the binding of Flt-3 ligand protein to Flt-3 receptor or the stimulation of dendritic precursor cells in a proliferation assay. Another embodiment of the present invention is a method to identify a compound capable of inhibiting CD40 function. Such a method includes the steps of (a) contacting an isolated CD40 protein of the present invention, with a putative inhibitory compound under conditions in which, in the absence of the compound, the CD40 protein binds to a CD40 binding partner (e.g., CD154) and (b) determining if the putative inhibitory compound inhibits the binding of CD40 protein to the CD40 binding partner. A CD40 binding partner is a molecule that selectively binds to CD40 protein. Likewise, a binding partner for any other immunoregulatory protein of the present invention includes molecules that selectively bind to that particular immunoregulatory protein. Another embodiment of the present invention is a method to identify a compound capable of inhibiting CD154 function. Such a method includes the steps of (a) contacting an isolated CD154 protein of the present invention, with a putative inhibitory compound under conditions in which, in the absence of the compound, the CD154 protein binds to a CD154 binding partner (e.g., CD40) and (b) determining if the putative inhibitory compound inhibits the binding of CD154 protein to the CD154 binding partner. Yet another embodiment of the present invention is a method to identify a compound capable of inhibiting IL-5 function. Such a method includes the steps of: (a) contacting an isolated IL-5 protein of the present invention, with a putative inhibitory compound under conditions in which, in the absence of the compound, the IL-5 protein binds to IL-5 receptor or stimulates T cells in a T cell proliferation assay, and (b) determining if the putative inhibitory compound inhibits the binding of IL-5 protein to IL-5 receptor or the stimulation of T cells in a T cell proliferation assay. Another embodiment of the present invention is a method to identify a compound capable of inhibiting IL-13 function. Such a method includes the steps of: (a) contacting an isolated IL-13 protein of the present invention, with a putative inhibitory compound under conditions in which, in the absence of the compound, the IL-

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13 protein binds to IL-13 receptor or stimulates T cells in a T cell proliferation assay, and (b) determining if the putative inhibitory compound inhibits the binding of IL-13 protein to IL-13 receptor or the stimulation of T cells in a T cell proliferation assay. Another embodiment of the present invention is a method to identify a compound

5 capable of inhibiting IFN α function. Such a method includes the steps of: (a) contacting an isolated IFN α protein of the present invention, with a putative inhibitory compound under conditions in which, in the absence of the compound, the IFN α protein binds to IFN α receptor or inhibits proliferation of GM-CSF stimulated TF-1 cells, and (b) determining if the putative inhibitory compound inhibits the binding of IFN α protein to

10 IFN α receptor or inhibits proliferation of GM-CSF stimulated TF-1 cells. Another embodiment of the present invention is a method to identify a compound capable of inhibiting GM-CSF function. Such a method includes the steps of: (a) contacting an isolated GM-CSF protein of the present invention, with a putative inhibitory compound under conditions in which, in the absence of said compound, the GM-CSF protein binds

15 to GM-CSF receptor or stimulates T cells in a T cell proliferation assay, and (b) determining if the putative inhibitory compound inhibits the binding of GM-CSF protein to GM-CSF receptor or the stimulation of T cells in a T cell proliferation assay.

Putative inhibitory compounds to screen include small organic molecules, antibodies (including mimetopes thereof), and/or ligand analogs. Such compounds are

20 also screened to identify those that are substantially not toxic in host animals.

Preferred IL-4, Flt-3 ligand, CD40, CD154, IL-5, IL-13, IFN α , and/or GM-CSF, proteins to inhibit are those produced by dogs, cats, horses or humans, even more preferred IL-4, Flt-3 ligand, CD40, CD154, IL-5, IL-13, IFN α , and/or GM-CSF proteins to inhibit are those produced by domestic dogs or cats. A particularly preferred inhibitor

25 of the present invention is capable of regulating an immune response in an animal. It is also within the scope of the present invention to use inhibitors of the present invention to target diseases involving undesired immune activity in animals. Compositions comprising inhibitors of IL-4, Flt-3 ligand, CD40, CD154, IL-5, IL-13, IFN α , and/or GM-CSF function can be administered to animals in an effective manner to regulate the

30 immune response in the animals, and preferably to prevent autoimmune disease, allergy, infectious disease, inflammation or prevent graft rejection in animals, or to treat animals

with such diseases. Effective amounts and/or dosing regimens can be determined using techniques known to those skilled in the art.

It is also within the scope of the present invention to use isolated proteins, mimetopes, nucleic acid molecules and/or antibodies of the present invention as
5 diagnostic reagents. Methods to use such diagnostic reagents are well known to those skilled in the art, see, for example, Janeway, et al., *ibid.*, and/or PCT Publication No. WO 98/23964, published June 4, 1998.

The following examples are provided for the purposes of illustration and are not intended to limit the scope of the present invention.

10 EXAMPLES

It is to be noted that the examples include a number of molecular biology, microbiology, immunology and biochemistry techniques considered to be familiar to those skilled in the art. Disclosure of such techniques can be found, for example, in Sambrook et al., *ibid.* and Ausubel, et al., 1993, *Current Protocols in Molecular*
15 *Biology*, Greene/Wiley Interscience, New York, NY, and related references.

Example 1

This example describes the isolation and sequencing of canine interleukin-4 (IL-4) nucleic acid molecules of the present invention. This example also describes expression of recombinant canine IL-4 in *E. coli* and mammalian cells; development of
20 monoclonal and polyclonal antibodies to *E. coli* expressed canine IL-4; and bioactivity of mammalian-expressed canine IL-4.

A. Isolation and sequencing of a canine IL-4 nucleic acid molecule.

Initial attempts to isolate a canine IL-4 nucleic acid molecule using various primers corresponding to putative conserved regions of IL-4 nucleic acid molecules
25 failed. Forward and reverse primers were then designed using a sequence tag site (IL-4sts) described by Venta et al. in GenBank. The forward primer was designated as IL-4stsA, having the nucleic acid sequence 5' CTATTAATGG GTCTCACCTC CCAA CT 3', designated herein as SEQ ID NO:11. The reverse primer was designated as prIL-4stsB, having the nucleic acid sequence 5' TCAACTCGGT GCACAGAGTC
30 TTGG 3', designated herein as SEQ ID NO:12. The primers were used to amplify PCR products from a *C. familiaris* mitogen activated T cell cDNA library that was

constructed in the Uni-ZAP® XR vector (available from Stratagene Cloning Systems, La Jolla, CA), using Stratagene's ZAP-cDNA® Synthesis Kit and the manufacturer's protocol. The mRNA was isolated from *C. familiaris* peripheral blood mononuclear cells about 4 hours after they were activated by a polyclonal activating agent in culture.

- 5 Four PCR products were produced that had the expected size range. The PCR products were cloned and sequenced using standard techniques. A portion of one of the four products was found to be somewhat homologous with an IL-4 nucleic acid sequence reported in GenBank.

To identify a cDNA encoding a full-length canine IL-4 protein, the PCR product
10 showing some homology with the IL-4 sequence reported in GenBank was used to generate an about 549 base pair DNA fragment as follows. The PCR product was labeled with ³²P and used as a probe to screen the canine PBMC cDNA library. Hybridization was done at about 6X SSC, 5X Denhardt's solution, 0.5 % SDS, 100 μg/ml of ssDNA and 100 μg/ml of tRNA, at about 68°C, for about 36 hr. (the
15 compositions of SSC and Denhardt's are described in Sambrook et al., *ibid.*). The filters were washed 3 times, for about 30 minutes per wash, at about 55° C in about 2X SSC, 0.2% SDS, followed by a final wash of about 30 minutes in the same buffer except using about 1X SSC. Positive clones were isolated and the cDNA inserts were sequenced for both strands using vector flanking primers and gene-specific internal primers. Sequence
20 analysis was performed using the GAP program of GCG (available from the University of Wisconsin) using the alignment settings of: gap weight set at 50, length weight set at 3, and average match set at 10 for nucleic acid sequence comparisons; and gap weight set at 12, length weight set at 4, and average match set at 2.912 for amino acid sequence comparisons.

- 25 A cDNA nucleic acid molecule was isolated, referred to herein as nCaIL-4₅₄₉, the coding strand of which was shown to have a nucleic acid sequence denoted herein as SEQ ID NO:1. The complement of SEQ ID NO:1 is represented herein by SEQ ID NO:3. Translation of SEQ ID NO:1 suggests that nucleic acid molecule nCaIL-4₅₄₉ encodes a full-length IL-4 protein of about 132 amino acids, denoted herein as
30 PCaIL-4₁₃₂, the amino acid sequence of which is presented in SEQ ID NO:2, assuming an open reading frame having an initiation codon spanning from nucleotide 43 through

nucleotide 45 of SEQ ID NO:1 and a stop codon spanning from nucleotide 439 through nucleotide 441 of SEQ ID NO:1. The coding region encoding PCaIL-4₁₃₂ is presented herein as nCaIL-4₃₉₆, which has the nucleotide sequence SEQ ID NO:4 (the coding strand) and SEQ ID NO:5 (the complementary strand). A putative signal sequence
 5 coding region extends from nucleotide 43 through nucleotide 114 of SEQ ID NO:1. The proposed mature protein (i.e., canine IL-4 protein from which the signal sequence has been cleaved), denoted herein as PCaIL-4₁₀₈, contains about 108 amino acids, extending from residue 25 through residue 132 of SEQ ID NO:2; PCaIL-4₁₀₈ amino acid sequence is represented herein as SEQ ID NO:20. The nucleic acid molecule encoding PCaIL-4₁₀₈
 10 is denoted herein as nCaIL-4₃₂₄, extending from nucleotide 115 through nucleotide 438 of SEQ ID NO:1. nCaIL-4₃₂₄ has a coding sequence denoted SEQ ID NO:19 and a complementary sequence denoted SEQ ID NO:21.

Comparison of nucleic acid sequence SEQ ID NO:1 with nucleic acid sequences reported in GenBank indicates that SEQ ID NO:1 showed the most homology, i.e., about
 15 89.3% identity, with a feline IL-4 gene. Comparison of amino acid sequence SEQ ID NO:2 with amino acid sequences reported in GenBank indicates that SEQ ID NO:2 showed the most homology, i.e., about 82.6% identity, with a feline IL-4 protein. Sequence analysis was performed using the GCG GAP program as described above.

B. Expression of recombinant canine IL-4 in *E. coli* and mammalian cells

20 i. *E. coli* expression

A recombinant molecule capable of expressing the mature form of canine IL-4, denoted herein as pGEX-nCaIL-4₃₂₇, was produced as follows. A 340-nucleotide fragment was PCR amplified from nucleic acid molecule nCaIL-4₅₄₉ (having coding strand SEQ ID NO:1) using the following primer sequences: positive strand 5'
 25 TGAATTCGGA CATAACTTCA ATATTAC 3' (SEQ ID NO:38) (*Eco*RI site in bold) and 5' TCTCGAGATT CAGCTTCATG CCTGTA 3' (SEQ ID NO:39) (*Xho*I site in bold). The resulting 340-base pair fragment was digested with *Eco*RI and *Xho*I restriction enzymes (available from New England Biolabs, Beverly, MA), according to the manufacturer's directions, and gel-purified using standard techniques. The digested
 30 340-base pair fragment, now 327 base pairs, was then ligated into pGEX-6P-1 (available from Amersham Pharmacia, Piscataway, NJ), which had been previously digested with

EcoRI and *XhoI* and gel purified, to produce recombinant molecule pGEX-nCaIL-4₃₂₇. Recombinant molecules of pGEX produce the protein of interest as a glutathione s-transferase (GST) fusion protein. The recombinant molecule pGEX-nCaIL-4₃₂₇ was transformed into DH5alpha cells (available from Life Technologies, Gaithersburg, MD), a recombination deficient strain of *E. coli*, to produce recombinant cell DH5-pGEX-nCaIL-4₃₂₇. The recombinant cells were screened for presence of insert by PCR and confirmed by enzyme restriction analysis and nucleic acid sequencing, using standard techniques. Several clonal recombinant molecules were transformed into BL21 cells (available from Amersham Pharmacia, Piscataway, NJ), a protease deficient strain of *E. coli*, to produce recombinant cell BL21-pGEX-nCaIL-4₃₂₇. These recombinant cells were screened, and the clone with the highest level of protein yield was selected for scaling up for larger-scale protein production. The resultant recombinant protein is referred to herein as *E. coli*PCaIL-4₁₀₉.

To produce and purify *E. coli*PCaIL-4₁₀₉, bacterial cultures of recombinant cell BL21:pGEX-nCaIL-4₃₂₇ were grown in shake flasks at 37°C and induced with 0.1 mM IPTG (isopropyl-β-D-thiogalactopyranoside), (available from Sigma Chemical Company, St. Louis, MO) when OD_{600nm} reached about 0.8 units. Growth was allowed to continue for about 4 hours; then bacteria were harvested by centrifugation at 4000 x g (times gravity) for 20 minutes. The bacterial pellet was washed and resuspended in phosphate buffered saline (PBS) (for recipe, see Sambrook et al, *ibid.*), then lysed by exposure to gaseous nitrogen pressure in a Parr pressure vessel (available from Parr Instrument Co., Moline, IL), according to the manufacturer's instructions. Cell debris was removed by centrifugation at 10,000 x g for 20 minutes. The IL-4-GST fusion protein *E. coli*PCaIL-4₁₀₉ was purified from the supernatant by allowing incubation with glutathione-conjugated resin, removing unbound proteins and then removing the GST tag with PRESCISSIION™ protease; all reagents were available from Amersham Pharmacia and all were used according to the manufacturer's directions.

Concentration and purity of *E. coli*PCaIL-4₁₀₉ were estimated by BCA Protein Assay kit (available from Pierce, Rockford, IL) and SDS-PAGE followed by Coomassie staining, respectively. The purified material exhibited a single band of approximately 14 kilodaltons (kD) by Coomassie stained SDS-PAGE.

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ii. CHO cell expression

A recombinant molecule denoted herein as pCMV-nCaIL-4₃₉₉, capable of expressing a full length form of canine IL-4 (including signal sequence) was produced as follows. A 422-nucleotide fragment was PCR amplified from nucleic acid molecule nCaIL-4₅₄₉ using the following primers: 5' CCCAAGCTTA TGGGTCTCACC TCCCAAC (*Hind*III site in bold), denoted SEQ ID NO:40, and 3' CCTCGAGATT CAGCTTTCAA TGCCTGTA (*Xho*I site in bold), denoted SEQ ID NO:127. The 422-base pair PCR product was digested with the restriction endonucleases *Hind*III and *Xho*I, both available from New England Biolabs. The resulting 399-base pair product encoding full-length canine IL-4 was gel purified using standard techniques and ligated into the cytomegalovirus (CMV) immediate-early transcription control region of the pCMV-Int A plasmid vector that had been digested with *Hind*III and *Xho*I (available from New England Biolabs), and gel purified, to produce the recombinant molecule pCMV-nCaIL-4₃₉₉. The pCMV-Int A plasmid vector was generated as referenced by J.E. Osorio et al., 1999, *Vaccine* 17, 1109-1116. Briefly, vector pRc/RSV, (available from Invitrogen Corp., San Diego, CA) was cleaved with restriction enzyme *Pvu*II (available from New England Biolabs), and the 2963-base pair *Pvu*II fragment was gel purified. The fragment was self-ligated to form the vector pRc/RSV(*Pvu*), which contains a Rous Sarcoma Virus (RSV) long terminal repeat, a multiple cloning site, a bovine growth hormone polyadenylation sequence, a bacterial origin of replication, and an ampicillin resistance gene. Vector pRc/RSV(*Pvu*) was restriction enzyme digested using *Hind*III and *Nru*I. A *Hind*III/*Ssp*I fragment containing the HCMV intermediate early promoter and first intron (i.e. intron A) was ligated into the digested pRc/RSV(*Pvu*) vector to produce the vector pCMV-Int A.

Stable expression of CaIL-4 in mammalian cells was carried out by transfecting the recombinant molecule pCMV-nCaIL-4₃₉₉ into Chinese Hamster Ovary cells, (CHO, available from ATCC) as follows. Six-well polystyrene tissue culture plates (available from Corning Costar, Acton, MA) were seeded with approximately 5 x 10⁵ cells/well in 2 milliliter (ml) cell culture media, consisting of Minimal Essential Media (MEM) supplemented with 100 mM L-glutamine, 100 mM gentamicin, and 10% fetal bovine serum (FBS), (all available from Life Technologies). Cells were grown to about 80%

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confluence (for about 18 hours) before transfection. The recombinant molecules to be transfected were purified using the Plasmid Midi Kit (available from Qiagen, Valencia, CA) and used according to the manufacturer's instructions. The recombinant molecule pCMV-nCaIL-4₃₉₉ was linearized using the restriction enzyme *PvuI* (available from New England Biolabs). The plasmid pcDNA3, (available from Invitrogen), which contains the neomycin resistance gene, was linearized using the restriction enzyme *EcoRI*. Approximately 2 μ g of pCMV-nCaIL-4₃₉₉ was mixed with about 2 ng of linearized pcDNA3 in about 100 μ l OPTIMEM™ media, available from Life Technologies. About 10 μ l Lipofectamine, (available from Life Technologies) was mixed with 100 μ l OPTIMEM. The nucleic acid molecule-containing mixture was then added to the Lipofectamine mixture and incubated at room temperature for about 45 minutes. After incubation, about 0.8 ml OPTIMEM was added, and the mixture was overlaid onto the CHO cells which had been previously rinsed with OPTIMEM. Cells were incubated for about 5 hours at 37°C 5% CO₂, 95% relative humidity. Approximately 1 ml of cell culture media as described previously, with 20% FBS, was added and the cells were incubated overnight. The media was changed at 24 hours, and at 72 hours post transfection, the cells were split 1:4 and put into fresh cell culture media containing about 500 μ g/ml geneticin (G418, available from Life Technologies). The media was changed every 3-5 days. After several weeks, G418 resistant colonies were trypsinized using sterile filter papers, 5-6 mm in diameter that were soaked in trypsin, which were then placed over individual wells of 24 well plates that contained separated widely spaced colonies of CHO cells. After 3 days, the papers were removed. The resulting recombinant cells are referred to herein as CHO-pCMV-nCaIL-4₃₉₉. The recombinant cells were then expanded and tested for the presence of nIL-4₃₉₉ RNA by RT-PCR and tested for the presence of PCaIL-4₁₃₃ protein by Western blot analysis. Westerns were developed with rabbit anti-*E. coli*PCaIL-4₁₀₉ serum and 607.1 monoclonal antibody, a monoclonal antibody that selectively binds to *E. coli*PCaIL-4₁₀₉ protein. See Example 1C for a description of how these antibodies were produced.

C. Monoclonal and polyclonal antibodies to recombinant canine IL-4 (i.e., anti-canine IL-4 antibodies)

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The following describes the development of monoclonal and polyclonal antibodies that selectively bind to *E. coli*PCaIL-4₁₀₉.

Female Balb/C mice, 6-8 weeks old, were injected subcutaneously, at about 4 sites, with a total of 25 μ g *E. coli*PCaIL-4₁₀₉ (produced as described in Example 1Bi) in Freund's Complete Adjuvant (day 0). Fourteen days later, the mice received an intraperitoneal boost of 25 μ g *E. coli*PCaIL-4₁₀₉ in Freund's Incomplete Adjuvant (day 14). Fourteen days later, serum was tested for antibody titer to *E. coli*PCaIL-4₁₀₉ by ELISA (day 28). Three days prior to fusion, mice were boosted intravenously with 20 μ g *E. coli*PCaIL-4₁₀₉ in PBS (day 35). Splenocytes were harvested from mice demonstrating the highest serum titer by ELISA and depleted of CD4+ and CD8+ cells. This depletion was achieved by incubation of the splenocytes with biotinylated rat anti-mouse CD4 and anti-mouse CD8 monoclonal antibodies, available from PharMingen, San Diego, CA. Antibody-labeled cells were then removed by incubation with M-280 streptavidin coated magnetic beads, available from Dynal, Oslo, Norway. Depleted splenocytes were fused to SP2/0 cells (available from ATCC) using 50% polyethylene glycol in unsupplemented Iscove's Modified Dulbecco's Media (IMDM), following established protocols; see, for example, Harlow E., and Lane D., eds., 1995, *Antibodies. A Laboratory Manual*, Monoclonal Antibodies, Cold Spring Harbor Laboratories; Harlow et al, *ibid*. Fused cells were plated in 96-well plates using IMDM cell culture media, (available from Life Technologies, Inc., Rockville, MD), which was supplemented with 10% fetal bovine serum, 2 mM L-glutamine, 1 mM sodium pyruvate, 1 X nonessential amino acids, 1 X MEM amino acids, 0.05 mg/ml gentamicin, and 0.5 mM β -mercaptoethanol (all reagents available from Life Technologies). Additionally, 100 μ M hypoxanthine, 0.4 μ M aminopterin, and 16 μ M thymidine, all available from Sigma Chemical Corporation, St Louis, MO, were added.

After about 7 days, wells positive for hybridoma growth were screened by ELISA to *E. coli*PCaIL-4₁₀₉. Immulon II 96-well plates (available from VWR, Denver, CO) were coated, overnight, with 100 ng/ml *E. coli*PCaIL-4₁₀₉ in 0.1 M carbonate/bicarbonate buffer, Ph 9.6. After blocking the wells with 20% FBS in Tris buffered saline (TBS), culture supernatants were allowed to bind. Presence of anti-*E. coli*PCaIL-4₁₀₉ mouse antibody was detected with polyclonal goat anti-mouse IgG conjugated to horseradish

peroxidase, (available from KPL, Gaithersburg, MD), and color developed with 3,3',5,5'-tetramethylbenzidine dihydrochloride (TMB), available from Pierce, Rockford, IL. Specificity of the ELISA reactivity was verified by Western blot analysis to *E. coli*PCaIL-4₁₀₉, developed with polyclonal goat anti-mouse IgG conjugated to alkaline phosphatase and nitro-blue tetrazolium/5-bromo-4-chloro-3'-indolyphosphate p-toluidine salt substrate (NBT/BCIP, available from Sigma). Western blots exhibited a single band of approximately 14 kD. Immunoglobulin isotype of the monoclonal antibodies was determined using IsoStrips, available from Boehringer Mannheim, Indianapolis, IN. Twenty-three monoclonal antibodies were generated to *E. coli*PCaIL-4₁₀₉, 22 of which were of the IgM isotype and one of which was IgG1, and is referred to herein as 607.1.

Polyclonal rabbit serum was produced by repeated immunization (over a 10 month period) of a male, New Zealand White rabbit 12-16 months old. Initial immunization was 50 ug *E. coli*PCaIL-4₁₀₉ (prepared as described in Example 1bi) in Freund's Complete Adjuvant, at several sites subcutaneously and intradermally. One month later, and at one month intervals thereafter, the rabbit was boosted intradermally with 50 ug *E. coli*PCaIL-4₁₀₉ in Freund's Incomplete Adjuvant. Serum was collected bi-weekly and titers monitored by ELISA and Western blot to *E. coli*PCaIL-4₁₀₉. Serum that selectively bound to *E. coli*PCaIL-4₁₀₉ protein is referred to as anti-*E. coli*PCaIL-4₁₀₉ serum.

D. Bioactivity of mammalian-expressed canine IL-4

The following describes a bioassay to detect the expression of canine IL-4 protein expressed in the supernatants from CHO-pCMV-nCaIL-4₃₉₉ recombinant cells by screening for production of CD23.

About 100 μ l Ramos cells, available from ATCC, at a concentration of about 3.5×10^3 cells/ml were seeded into 96-well flat bottom plates, available from Becton Dickinson, Franklin Lakes, NJ). These cells were grown in RPMI media supplemented with 100 mM L-glutamine, gentamicin, and 10 % FBS (called TCM). The Ramos cells were then treated in 5% CO₂ for 37°C for approximately 48 h. with one of the following:

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Group	Treatment
1	TCM
2	CHO-pCMV (a transfectant cell line containing the empty pCMV vector) supernatant (1:4 final dilution in TCM)
3	CHO-pCMV-nCaIL-4 ₃₉₉ supernatant (1:20 final dilution in TCM)

5 Triplicate samples for each treatment group were pooled for staining to look for increased expression of CD23 (one of the reported effects of IL-4). Briefly, 1×10^5 cells from each treatment group were incubated in phosphate buffered saline (PBS) containing 30% FBS for 15-30 min on ice. The cells were collected and incubated with the following:

10	<u>Condition</u>	<u>Primary Incubation</u>	<u>Secondary Incubation</u>
	A	PBS	Goat anti mouse PE
	B	Mouse anti human CD23	Goat anti mouse PE

Mouse anti-human CD23 monoclonal antibody, available from Pharmingen, was used at about 10 $\mu\text{g/ml}$. Goat (Fab'2) anti mouse IgG PE, available from Southern
 15 Biotechnologies was used at about 2.5 $\mu\text{g/ml}$. These reagents were diluted in PBS with 5% FBS. Primary incubations were performed for 30-60 minutes on ice, and secondary incubations were performed for 20-30 min on ice. Three washes of PBS/5% FBS were performed in between each incubation. Cells were then analyzed on a flow cytometer (e.g., MoFlow Desk Top System, available from Cytomation, Ft. Collins, CO) with the
 20 fluorescein gate set at 10^1 . The results are shown below in Table 2.

Table 2. Induction of CD23 on Ramos cells post-treatment with supernatants from CHO-pCMV-nCaIL-4₃₉₉.

Treatment	Condition	% positive
1	A	0
	B	1
2	A	8
	B	1
3	A	3

25

Table 2 shows that the canine IL-4 expressed by the CHO transfectant CHO-pCMV-nCaIL-4₃₉₉ is biologically active, demonstrated by its ability to induce expression of CD23 in Ramos cells.

Example 2

5 This example describes the isolation and sequencing of certain canine Flt-3 ligand and feline Flt-3 nucleic acid molecules and proteins of the present invention. The example also describes expression of a canine Flt-3 ligand protein of the present invention in CHO cells, as well as detection of the expressed canine Flt-3 ligand protein.

A. Canine Flt-3 ligand nucleic acid molecules and proteins.

10 i. This example describes the isolation and sequencing of certain canine Flt-3 ligand nucleic acid molecules and proteins of the present invention.

A canine Flt-3 ligand nucleic acid molecule was produced as follows. A pair of primers was initially used to amplify DNA from the *C. familiaris* mitogen activated PBMC cDNA library described above in Example 1. A forward primer referred to as
15 FLT3F1, having the nucleic acid sequence 5' CTGGCGCCAG CCTGGAGCCC 3', designated herein as SEQ ID NO:13 was used in combination with a reverse primer referred to herein as FLT3B1, having the nucleic acid sequence 5' GGGAGATGTT GGTCTGGACG 3', referred to herein as SEQ ID NO:14 to amplify Flt-3 ligand DNA from the cDNA library by polymerase chain reaction (PCR). The primers were designed
20 using conserved regions of IL-4 cDNA sequences from other species in the public databases corresponding to the positions shown below:

	Database	Accession number	Nucleotides	Animal
	gb	U04806	102-121	human
	gb	L23636	41-60	mouse
25	gb	U04806	77-458	human
	gb	L23636	419-400	mouse

A 360-base pair (bp) PCR product was generated in the above reaction that was purified, radiolabeled and used as a probe to screen the cDNA library. Hybridization
30 was performed in 6X SSC, 5X Denhardt's solution, 0.5 % SDS, 100 µg/ml ssDNA and 100 µg/ml of tRNA, at 68°C, for about 36 h. The filters were washed 3 times, for about

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30 minutes per wash, at 55°C in 2X SSC, 0.1% SDS, followed by a final wash in 0.25X SSC, for about 30 minutes, at 55° C. Several positive phage clones were identified and shown to produce PCR products when used as templates in combination with the FLT3F1 and FLT3B1 primers. The DNA inserts in the phage clones were sequenced
 5 using standard techniques and failed to yield any clones containing DNA inserts having a portion homologous to published Flt-3 ligand sequences. The 360-bp PCR fragment generated above was then cloned into the vector pcDNA 2.1 (available from Invitrogen Corp., San Diego, CA). Several independent colonies were generated and the sequences of their inserts determined. One clone was identified that which contained insert
 10 sequence having a portion that was somewhat homologous to published human or murine Flt-3 ligand sequence.

Two canine Flt-3 ligand-specific primers were then designed using the nucleic acid sequence obtained using the 360-bp PCR product described above.

	<u>Primer</u>	<u>Sequence</u>	<u>SEQ ID NO</u>
15	DFLB1	5' GACCAGGCGCCAGAACGC 3'	SEQ ID NO:15
	DFLF1	5' CGGTCACCATCCGCAAGC 3'	SEQ ID NO:16

The 5' region of a Flt-3 ligand nucleic acid molecule was PCR amplified from the cDNA library using the DFLB1 primer in combination with the 5' T3 vector primer from the Uni-ZAP® XR vector (available from Stratagene). The 3' region of a Flt-3 ligand
 20 nucleic acid molecule was PCR amplified from the cDNA library using the DFLF1 in combination with the 3' T7 primer from the Uni-ZAP® XR vector (available from Stratagene). A 855-bp PCR product was obtained representing the 5' region of a Flt-3 ligand nucleic acid molecule. A 265-bp PCR product was obtained representing the 3' region of a Flt-3 ligand nucleic acid molecule. Both the 855-bp PCR product and
 25 265-bp PCR product were cloned and sequenced using standard methods. Additional canine Flt-3 ligand-specific primers were designed using the nucleic acid sequence obtained from the sequence of the 855-bp PCR product and 265-bp PCR products.

<u>Primer</u>	<u>Sequence</u>	<u>SEQ ID NO</u>
DFLB2	5' TGGCAAGGCAGTGGCCTC 3'	SEQ ID NO:17

DFLF2 5' GCCGAGATGATAGTGCTGGC 3' SEQ ID NO:18

A 546-bp PCR product was generated using the primer DFLF2 in combination with the primer DFLB2 to amplify a PCR product from the cDNA library. The 546-bp PCR product was then purified, radiolabelled and used as a probe to screen the cDNA library. Hybridization was performed in 6X SSC, 5X Denhardt's solution, 0.5 % SDS, 100 μ g/ml of ssDNA and 100 μ g/ml of tRNA, at 68°C, for about 36 hr. The filters were washed in 1.25X SSC, for about 30 minutes, at 55°C. Four cDNA clones encoding full-length canine Flt-3 ligand were isolated. Nucleic acid sequence was obtained using standard techniques.

10 A Flt-3 ligand clone was isolated, referred to herein as nCaFlt3L₁₀₁₃, the coding strand of which was shown to have a nucleic acid sequence denoted herein as SEQ ID NO:6. The complement of SEQ ID NO:6 is represented herein by SEQ ID NO:8. Translation of SEQ ID NO:6 suggests that nucleic acid molecule nCaFlt3L₁₀₁₃ encodes a full-length Flt-3 ligand protein of about 294 amino acids, denoted herein as PCaFlt3L₂₉₄,
15 the amino acid sequence of which is presented in SEQ ID NO:7, assuming an open reading frame having an initiation codon spanning from nucleotide 35 through nucleotide 37 of SEQ ID NO:6 and a stop codon spanning from nucleotide 917 through nucleotide 919 of SEQ ID NO:6. The coding region encoding PCaFlt3L₂₉₄ is presented herein as nCaFlt3L₈₈₂, which has the nucleotide sequence SEQ ID NO:9 (the coding
20 strand) and SEQ ID NO:10 (the complementary strand). A putative signal sequence coding region extends from nucleotide 35 through nucleotide 112 of SEQ ID NO:6. The proposed mature protein (i.e., canine Flt-3 ligand protein from which the signal sequence has been cleaved), denoted herein as PCaFlt3L₂₆₈ (SEQ ID NO:23), contains about 268 amino acids, extending from residue 27 through residue 294 of SEQ ID NO:7. The
25 nucleic acid molecule encoding PCaFlt3L₂₆₈ is denoted herein as nCaFlt3L₈₀₄, extending from nucleotide 113 through nucleotide 916 of SEQ ID NO:6. nCaFlt3L₈₀₄ has a coding sequence denoted SEQ ID NO:22 and a complementary sequence denoted SEQ ID NO:24.

Below is a description of the identification of alternatively spliced *Canis* Flt3
30 ligand transcripts. Besides cDNA clones such as nucleic acid molecule nCaFlt3L₁₀₁₃

encoding the full-length canine Flt3 ligand protein, two splice variants of canine Flt3 ligand cDNA clones were also isolated, using the same hybridization conditions as mentioned previously in this Example. One such variant (Clone 1), denoted herein as nCaFlt3L₉₈₅, has a coding strand the nucleic acid sequence of which is represented as

5 SEQ ID NO:25. The complement of SEQ ID NO:25 is represented herein by SEQ ID NO:27. Translation of SEQ ID NO:25 suggests that nucleic acid molecule nCaFlt3L₉₈₅ encodes a Flt-3 ligand protein of 276 amino acids, denoted herein as PCaFlt3L₂₇₆, the amino acid sequence of which is represented by SEQ ID NO:26, assuming an open reading frame having an initiation codon spanning from nucleotide 74 through

10 nucleotide 76 of SEQ ID NO:25 and a stop codon spanning from nucleotide 902 through nucleotide 904 of SEQ ID NO:25. The coding region encoding PCaFlt3L₂₇₆ is represented herein as nCaFlt3L₈₂₈, which has the nucleotide sequence SEQ ID NO:28 (the coding strand) and SEQ ID NO:29 (the complementary strand). Alignment of nucleic acid molecules nCaFlt3L₈₈₂ and nCaFlt3L₈₂₈ indicates that the nucleic acid

15 molecules are identical except for a deletion in nCaFlt3L₈₂₈, which spans from nucleotide 343 through nucleotide 396 of nCaFlt3L₈₈₂. Accordingly, nCaFlt3L₈₂₈ encodes 18 fewer amino acids than nCaFlt3L₈₈₂. The deletion in PCaFlt3L₂₇₆, which spans from residue 115 through residue 132 of PCaFlt3L₂₉₄, occurs between helix III and helix IV of the canine Flt3 ligand protein inferred from alignment with the human and

20 mouse Flt3 ligand protein (Lyman et al., *Cell*, vol. 75, pp. 1157-1167, 1993; Hannum et al., *Nature*, vol. 368, pp. 643-648, 1994; Lyamn et al., *Blood*, vol. 83, pp. 2795-2801, 1994). In addition, the alignment shows that there are 39 more nucleotides in the 5' untranslated region of nucleic acid molecule nCaFlt3L₉₈₅ (nucleotides 1 to 39) than nucleic acid molecule nCaFlt3L₁₀₁₃ and there are 2 more nucleotides in the 3'

25 untranslated region of nucleic acid molecule nCaFlt3L₉₈₅ (nucleotides 922 to 923) than nucleic acid molecule nCaFlt3L₁₀₁₃. The remaining sequences between nCaFlt3L₉₈₅ and nCaFlt3L₁₀₁₃ are identical. A putative mature form of nCaFlt3L₉₈₅ (without the signal

sequence) is predicted. The putative signal sequence coding region extends from nucleotide 74 to nucleotide 151 of SEQ ID NO:25. The proposed mature protein, denoted herein as PCaFlt3L₂₅₀, represented by SEQ ID NO:31, contains about 250 amino acids, extending from residue 27 through residue 276 of SEQ ID NO:26. The nucleic acid molecule encoding PCaFlt3L₂₅₀, extending from nucleotide 152 through nucleotide 901 of SEQ ID NO:6, denoted herein as nCaFlt3L₇₅₀, is represented by SEQ ID NO:30 (the coding strand) and SEQ ID NO:32 (the complement strand).

A second variant (Clone 19) is represented by nucleic acid molecule nCaFlt3L₁₀₁₉, the coding strand of which is denoted herein as SEQ ID NO:33. The complement of SEQ ID NO:33 is denoted herein as SEQ ID NO:35. Translation of SEQ ID NO:33 suggests that nCaFlt3L₁₀₁₉ encodes a Flt-3 ligand protein of 31 amino acids, PCaFlt3L₃₁, denoted SEQ ID NO:34, assuming an initiation codon spanning from nucleotide 74 through nucleotide 76 and a stop codon spanning nucleotide 167 through nucleotide 169 of SEQ ID NO:33. The coding region encoding PCaFlt3L₃₁ is represented herein as nCaFlt3L₉₃, which has the nucleotide sequence SEQ ID NO:36 (the coding strand) and SEQ ID NO:37 (the complementary strand). Alignment of nucleic acid molecules nCaFlt3L₉₈₅ and nCaFlt3L₁₀₁₉ indicates the presence of an insertion of 91 nucleotides in nCaFlt3L₁₀₁₉. The insertion spans nucleotide 107 through nucleotide 198 of nCaFlt3L₁₀₁₉. A stop codon is found in this insertion in frame with the predicted initiation codon, which span nucleotide 74 through nucleotide 76 of SEQ ID NO:6. Since this insertion (with an in-frame stop codon) occurs in or close to the signal peptide, it is likely that nucleic acid molecule nCaFlt3L₁₀₁₉ encodes a nonfunctional Flt-3 ligand protein.

Comparison of nucleic acid sequence SEQ ID NO:6 with nucleic acid sequences reported in GenBank indicates that SEQ ID NO:6 showed the most homology, i.e., about 69.8% identity, with a human Flt-3 ligand gene. Comparison of amino acid sequence SEQ ID NO:7 with amino acid sequences reported in GenBank indicates that SEQ ID NO:7 showed the most homology, i.e. about 71% identity, with a human Flt-3 ligand protein. Sequence analysis was performed with DNAsis™ using the alignment settings of: gap penalty set at 5; number of top diagonals set at 5; fixed gap penalty set at 10; K-tuple set at 2; window size set at 5 and floating gap penalty set at 10.

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ii. This example describes the production of a recombinant molecule encoding a full length canine Flt-3 ligand protein and expression of that protein by a recombinant cell of the present invention.

A recombinant molecule, denoted herein as pCMV-nCaFlt3L₈₈₂ and capable of
5 expressing a full length form of Flt-3 ligand, was produced as follows. Nucleic acid molecule nCaFlt3L₈₈₂ was digested with the restriction endonucleases *EcoRI* and *XbaI*, gel purified and ligated into pCMV-Int A (prepared by methods described in Example 1) to produce recombinant molecule pCMV-nCaFlt3L₈₈₂. Insert size and identity were confirmed by restriction digestion, PCR, and sequencing analyses.

10 Stable transfectants expressing the recombinant molecule pCMV-nCaFlt3L₈₈₂ were established in Chinese Hamster Ovary cells (CHO, available from ATCC) as follows. Briefly, six-well polystyrene tissue culture plates were seeded with approximately 4×10^5 cells per well in 2 ml of MEM (available from Life Technologies, Gaithersburg, MD) supplemented with 100 mM L-glutamine, gentamicin, and 10% FBS
15 (TCM). Cells were grown to about 80% confluence (about 18 hr). The recombinant molecule to be transfected was prepared using the Qiagen Endotoxin-Free Plasmid Maxi Kit as per the manufacturer's instructions. The recombinant molecule was linearized with the restriction enzyme *PvuI*, extracted with phenol, and precipitated with isopropanol. The plasmid pcDNA 3, available from Invitrogen, which contains the
20 neomycin resistance gene, was linearized with the restriction enzyme *EcoRI*. Approximately 1 μ g of recombinant plasmid DNA and 100 ng of pcDNA3 were mixed with about 100 μ l OptiMEM medium, available from Life Technologies. About 10 μ l Lipofectamine (available from Life Technologies) was mixed with 100 μ l OptiMEM. The DNA-containing mixture was then added to the Lipofectamine mixture and
25 incubated at room temperature for about 30 min. After incubation, about 800 μ l of OptiMEM was added, and the entire mixture was overlaid onto the CHO cells that had been rinsed with OptiMEM. Cells were incubated for 6 hours at 37°C, 5% CO₂, 95% relative humidity. Approximately 1 ml of TCM with 20% FBS was added, and the cells were incubated overnight. The media was changed after about 24 hr. About 72 hr post
30 transfection, the cells were split 1:4 and put into selection TCM containing 500 μ g/ml Geneticin (G418), available from Life Technologies. The medium was changed every 3-

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5 days. After several weeks, G418-resistant colonies were trypsinized, and the cells were plated into 24 well plates. The resulting recombinant cells are referred to herein as CHO-pCMV-nCaFlt3L₈₈₂. The recombinant cells were then expanded for testing.

iii. The following describes the detection of expression of a canine Flt-3 ligand protein of the present invention by CHO-pCMV-nCaFlt3L₈₈₂, a recombinant cell of the present invention.

Recombinant cells CHO-pCMV-nCaFlt3L₈₈₂, produced as described in Example 2, part (B)(ii) above, were tested for surface expression of canine Flt-3 ligand using a cross-reactive goat anti-human Flt-3 ligand polyclonal antibody as follows. Briefly,
 10 1 x 10⁵ CHO-pCMV-nCaFlt3L₈₈₂ cells or CHO-pCMV cells (i.e., cells transfected with an empty vector as described in Example 1) were incubated in phosphate buffered saline (PBS) containing 30% fetal bovine serum (FBS) for about 30 min on ice. The cells were then spun down and treated with the following:

	<u>Condition</u>	<u>Primary Incubation</u>	<u>Secondary Incubation</u>
15	1	PBS	Rabbit (Fab'2) anti sheep (H+L) FITC
	2	Goat anti-human Flt3 ligand	Rabbit (Fab'2) anti sheep (H+L) FITC

Goat anti-human Flt3 ligand, available from R and D Systems, Minneapolis, MN was used at about 20µg/ml. Rabbit (Fab'2) anti sheep (H+L) FITC, available from Southern Biotechnology Associates, Inc., was used at about 10 µg/ml. These reagents were
 20 diluted in PBS/5%FBS. All incubations were in 50 µl for about 1 hr on ice with 2 washes of PBS/5%FBS in between each incubation. Cells were then analyzed on a flow cytometer (e.g., MoFlow Desk Top System, available from Cytomation, Ft. Collins, CO) with the fluorescein gate set at 10¹. The results are shown below in Table 3.

Table 3. Expression of canine Flt3 ligand on CHO transfectants.

Cells	% positive	
	Condition 1	Condition 2
CHO-pCMV	1	1
CHO-pCMV nCaFlt3L ₈₈₂	2	48
5 CHO-pCMV nCaFlt3L ₈₈₂	1	20

Table 3 shows that canine Flt3 ligand is expressed on the surface of the CHO transfectants.

B. Feline Flt-3 ligand nucleic acid molecules and proteins.

This example describes the production of certain feline Flt-3 ligand nucleic acid
 10 molecules and proteins of the present invention.

A nucleic acid molecule encoding a feline Flt 3 ligand was isolated from a feline PBMC cDNA library as follows. A *Felis catus* mitogen activated PBMC cDNA library was constructed in the Uni-Zap-R XR™ vector, available from Stratagene, La Jolla, Ca, using Stratagene's Zap-cDNA-R™ Synthesis Kit and the manufacturer's protocol using
 15 mRNA isolated from *F. catus* peripheral blood mononuclear cells about 4 hours after they were activated by a polyclonal activating agent in culture. PCR amplification to isolate a feline Flt 3 ligand nucleic acid molecule was conducted according to the following set of steps: one initial denaturation step at 95°C for 3 minutes; then 35 cycles of the following: 94°C for 30 seconds, 53.8°C for 30 seconds, and 72°C for 105
 20 seconds; then one final extension step at 72°C for 8 minutes. A 395-nucleotide cDNA fragment containing the 5' end of feline Flt3 ligand coding region, denoted nFeFlt3L₃₉₅, was amplified from the feline PMBC cDNA library using the following primers: vector primer T3 having nucleic acid sequence 5' AATTAACCCT CACTAAAGGG 3' (SEQ ID NO:142) (available from Stratagene) and the antisense primer having SEQ ID NO:14, described in Example 2A. The nucleic acid sequence of the coding strand of nFeFlt3L₃₉₅
 25 is denoted SEQ ID NO:41. A 793-nucleotide cDNA fragment containing the 3' end of feline Flt3 ligand coding region, denoted nFeFlt3L₇₉₃, was isolated using sense primer 2 having the nucleic acid sequence 5' CACAGYCCCA TCTCCTCC 3' (where Y was either T or C) denoted herein as SEQ ID NO:151, in conjunction with vector primer T7

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having the nucleic acid sequence 5' GTAATACGAC TCACTATAGG GC 3' (SEQ ID NO:152). The nucleic acid sequence of the coding strand of nFeFlt3L₇₉₃ is denoted SEQ ID NO:42. Nucleic acid molecules nFeFlt3L₃₉₅ and nFeFlt3L₇₉₃ overlap by 246 nucleotides and form a composite sequence encoding a Flt3 ligand protein that is similar in length to that of PCaFlt3L₂₉₄. This composite feline Flt3 ligand cDNA is referred to herein as nFeFlt3L₉₄₂, the coding strand of which was shown to have nucleic acid sequence SEQ ID NO:43. The reverse complement of SEQ ID NO:43 is referred to herein as SEQ ID NO:45. Translation of SEQ ID NO:43 suggests that nucleic acid molecule nFeFlt3L₉₄₂ encodes a Flt3 ligand protein of 291 amino acids, denoted herein as PFeFlt3L₂₉₁, the amino acid sequence of which is presented in SEQ ID NO:44, assuming an open reading frame having an initiation codon spanning from nucleotide 31 through nucleotide 33 of SEQ ID NO:43 and a stop codon spanning from nucleotide 904 through nucleotide 906 of SEQ ID NO:43. The coding region encoding PFeFlt3L₂₉₁, not including the termination codon, is presented herein as nFeFlt3L₈₇₃, which has the nucleotide sequence SEQ ID NO:46 (the coding strand) and SEQ ID NO:47 (the complementary strand). A putative signal sequence coding region extends from nucleotide 31 to nucleotide 108 of SEQ ID NO:43. The proposed mature protein, denoted herein as PFeFlt3L₂₆₅, denoted SEQ ID NO:49, contains about 265 amino acids, extending from residue 27 through residue 291 of SEQ ID NO:44. The nucleic acid molecule encoding PFeFlt3L₂₆₅ is denoted herein as nFeFlt3L₇₉₅, (SEQ ID NO:48) extending from nucleotide 109 through nucleotide 903 of SEQ ID NO:43. SEQ ID NO:48 has a complementary strand denoted SEQ ID NO:50.

Sequence alignment indicates that nucleic acid sequence SEQ ID NO:43 shares the highest (67.8%) identity with the nucleic acid sequence of human Flt-3 ligand (GenBank accession numbers U04806 and U03858). Amino acid sequence SEQ ID NO:44 shares the highest (70.2%) identity with human Flt-3 ligand protein (GenBank accession numbers U04806 and U03858).

Example 3.

This example describes the isolation and sequencing of certain canine CD40 and feline CD40 nucleic acid molecules and proteins of the present invention.

A. Canine CD40 nucleic acid molecules and proteins

This example describes the production of certain canine CD40 nucleic acid molecules and proteins of the present invention.

A canine CD40 nucleic acid molecule of the present invention was produced by PCR amplification as follows. A 321-nucleotide canine CD40 nucleic acid molecule, denoted nCaCD40₃₂₁, was amplified from a canine PBMC cDNA library, prepared as described in Example 1, using two degenerate oligonucleotide primers designed in accordance with conserved regions of human, bovine, rabbit, and mouse CD40 gene sequences available in GenBank: sense primer, 5' TGCCCRSTCG GCTTCTTCTC C 3', denoted herein as SEQ ID NO:128; and antisense primer, 5' CGACTCTCTT TRCCRTCCTC CTG 3', denoted herein as SEQ ID NO:129, where R was either A or G and S was either G or C. PCR conditions were as follows: one initial denaturation step at 95°C for 3 minutes; then 35 cycles of the following: 94°C for 30 seconds, then 53°C for 30 seconds, then 72°C for 105 seconds; followed by one final extension at 72°C for 5 minutes. The resulting PCR product, i.e., nCaCD40₃₂₁, with a coding strand represented by SEQ ID NO:51, was radiolabeled using standard techniques and used to screen the canine PBMC cDNA library, under the following hybridization conditions: hybridized in 6X SSC, 5X Denhardt's solution, 0.5% SDS, 100 µg/ml single stranded DNA, 100 µg/ml tRNA for 36 hours at 68°C, followed by a wash of 0.1% SDS, 1X SSC at 55°C for 60 minutes. A clone (Clone 18B) containing a 1425-nucleotide canine CD40 nucleic acid molecule, denoted nCaCD40₁₄₂₅, was obtained. The nucleic acid sequence of the coding strand of nCaCD40₁₄₂₅ is represented as SEQ ID NO:52. The reverse complement of SEQ ID NO:52 is referred to herein as SEQ ID NO:54. Translation of SEQ ID NO:52 suggests that nucleic acid molecule nCaCD40₁₄₂₅ encodes a canine CD40 protein of 274 amino acids, denoted herein as PCaCD40₂₇₄, the amino acid sequence of which is presented in SEQ ID NO:53, assuming an open reading frame having an initiation codon spanning from nucleotide 196 through nucleotide 198 of SEQ ID NO:52 and a stop codon spanning from nucleotide 1018 through nucleotide 1020 of SEQ ID NO:52. The coding region encoding PCaCD40₂₇₄, not including the termination codon, is presented herein as nCaCD40₈₂₂, which has the nucleotide sequence SEQ ID NO:55 (the coding strand) and SEQ ID NO:56 (the complementary strand).

A putative signal sequence coding region extends from nucleotide 196 through nucleotide 252 of SEQ ID NO:52. The proposed mature protein, denoted herein as PCaCD40₂₅₅, represented by SEQ ID NO:58, contains about 255 amino acids, extending from residue 20 through residue 274 of SEQ ID NO:53. The nucleotide sequence
5 encoding PCaCD40₂₅₅, which extends from nucleotide 253 through nucleotide 1017 of SEQ ID NO:52, is denoted herein as nucleic acid molecule nCaCD40₇₆₅, represented by SEQ ID NO:57 (the coding strand) and SEQ ID NO:59 (the complement strand).

Sequence analysis was performed with DNAsis™ using the alignment settings of: gap penalty set at 5; number of top diagonals set at 5; fixed gap penalty set at 10; k-
10 tuple set at 2; window size set at 5 and floating gap penalty set at 10. At the amino acid level, PCaCD40₂₇₄ shares 65.3%, 50.1%, and 42.3% identity with the CD40 proteins of human, bovine, and mouse, respectively (Stamenkovic et al., *EMBO J.*, vol. 8:1403-1410, 1989; Hirano et al., *Immunology*, vol. 90, pp. 294-300, 1997; Grimaldi et al., *J. Immunol.*, vol. 143, pp.3921-3926; Torres and Clark, *J. Immuno.*, vol. 148, pp. 620-626).
15 At the nucleotide level, nCaCD40₁₄₂₅ shares 69.3%, 69.4%, and 40.4% identity with the cDNA sequences of human, bovine, and mouse CD40, respectively.

B. Feline CD40 nucleic acid molecules and proteins

This example describes the isolation and sequencing of certain nucleic acid molecules of the present invention that encode certain feline CD40 proteins of the
20 present invention.

A 336-nucleotide feline CD40 nucleic acid molecule, denoted nFeCD40₃₃₆, was amplified from a feline PBMC cDNA library, prepared as described in Example 2, using PCR conditions and primers as described in Example 3A, i.e., a sense primer having SEQ ID NO:128; and an antisense primer having SEQ ID NO:129. The resulting PCR
25 product, i.e., nFeCD40₃₃₆, was shown to have a coding strand the nucleic acid sequence of which is represented as SEQ ID NO:60. The reverse complement of SEQ ID NO:60 is referred to herein as SEQ ID NO:62. Translation of SEQ ID NO:60 suggests that nucleic acid molecule nFeCD40₃₃₆ encodes a partial CD40 protein of 112 amino acids, denoted herein as PFeCD40₁₁₂, the amino acid sequence of which is presented in SEQ ID
30 NO:61, assuming an open reading frame spanning from nucleotide 1 through nucleotide 336 of SEQ ID NO:60.

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Comparison of nucleic acid sequence SEQ ID NO:60 with nucleic acid molecules reported in GenBank indicates that SEQ ID NO:60 showed the most homology, i.e. 67.2% identity, with a human CD40 gene. Comparison of amino acid sequence SEQ ID NO:61 with amino acid sequences reported in GenBank indicates that
5 SEQ ID NO:61 showed the most homology, i.e. about 54.4% identity, with a human CD40 protein. Sequence analysis was performed using the GCG GAP program as described above.

Example 4

This example describes the isolation and sequencing of certain canine CD154
10 (canine CD40 ligand) and feline CD154 (feline CD40 ligand) nucleic acid molecules and proteins of the present invention.

A. Canine CD154 (CD40 ligand) nucleic acid molecules and proteins

The following describes the isolation and sequencing of certain cDNA nucleic acid molecules encoding certain canine CD154 (CD40 ligand) proteins of the present
15 invention.

A canine CD154 nucleic acid molecule of the present invention was produced by PCR amplification as follows. A 390-nucleotide canine CD40 nucleic acid molecule, denoted nCaCD154₃₉₀, was amplified from a canine PBMC cDNA library, prepared as described in Example 1, using two degenerate oligonucleotide primers designed in
20 accordance with human CD154 gene sequences available in GenBank: sense primer, 5' CCTCAAATTG CGGCACATGT C 3', denoted herein as SEQ ID NO:130; and antisense primer, 5' CTGTTTCAGAG TTTGAGTAAG CC 3', denoted herein as SEQ ID NO:131. PCR conditions used for canine CD154 cDNA amplification were standard conditions for PCR amplification (Sambrook, et al., *ibid.*). The resulting PCR product,
25 i.e., nCaCD154₃₉₀, with a coding strand represented by SEQ ID NO:63, was radiolabeled using standard techniques and used to screen the canine PBMC cDNA library, under the hybridization conditions described in Example 3. A clone containing a 1878-nucleotide canine CD154 nucleic acid molecule, denoted nCaCD154₁₈₇₈, was obtained. The nucleic acid sequence of the coding strand of nCaCD154₁₈₇₈ is represented as SEQ ID NO:64.
30 The reverse complement of SEQ ID NO:64 is referred to herein as SEQ ID NO:66. Translation of SEQ ID NO:64 suggests that nucleic acid molecule nCaCD154₁₈₇₈

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encodes a CD154 protein of 260 amino acids, denoted herein as PCaCD154₂₆₀, the amino acid sequence of which is presented in SEQ ID NO:65, assuming an open reading frame having an initiation codon spanning from nucleotide 284 through nucleotide 286 of SEQ ID NO:64 and a stop codon spanning from nucleotide 1064 through nucleotide 1066 of SEQ ID NO:64. The coding region encoding PCaCD154₂₆₀, not including the termination codon, is presented herein as nCaCD154₇₈₀, which has the nucleotide sequence SEQ ID NO:67 (the coding strand) and SEQ ID NO:68 (the complementary strand).

A putative signal/membrane anchor sequence coding region extends from nucleotide 284 through nucleotide 430 of SEQ ID NO:64. The proposed soluble CD154 protein, denoted herein as PCaCD154₂₁₁, represented by SEQ ID NO:70, contains about 211 amino acids, extending from residue 50 through residue 260 of SEQ ID NO:65. The nucleotide sequence encoding PCaCD154₂₁₁, which extends from nucleotide 431 through nucleotide 1063 of SEQ ID NO:64, is denoted herein as nucleic acid molecule nCaCD154₆₃₃, represented by SEQ ID NO:69 (the coding strand) and SEQ ID NO:71 (the complement strand).

Sequence analysis was performed with DNAsis™ using the alignment settings of: gap penalty set at 5; number of top diagonals set at 5; fixed gap penalty set at 10; k-tuple set at 2; window size set at 5 and floating gap penalty set at 10. At the amino acid level, PCaCD154₂₆₀ shares 78.0%, 77.6%, and 67.6% identity with the CD154 proteins of human, bovine, and mouse, respectively (Graf et al., *Eur. J. Immunol.*, vol. 22, pp. 3191-3194, 1992; Hollenbaugh, et al., *EMBO J.*, vol. 11:4313-4321, 1992; Gauchat et al., *FEBS lett.*, vol., 315, pp. 259-266, 1993; Mertens et al., *Immunogenetics*, vol. 42, pp. 430-431; Armitage et al., *Nature*, vol. 357, pp. 80-82; 1992). At the nucleotide level, nCaCD154₁₈₇₈ shares 81.1%, 81.5%, and 74.4% identity with the sequences of human, bovine, and mouse CD154 cDNAs, respectively.

B. Feline CD154 (CD40 ligand) nucleic acid molecules and proteins

This example describes the isolation and sequencing of certain nucleic acid molecules encoding certain feline CD154 (CD40 ligand) proteins of the present invention.

A feline CD154 nucleic acid molecule was isolated by PCR amplification from a feline PBMC cDNA library, prepared as described in Example 2, using Amplitaq DNA polymerase (available from PE Applied Biosystems Inc, Foster City, CA) under the following PCR protocol: one initial denaturation step at 95°C for 5 minutes; then 40
5 cycles of the following: 94°C for 45 seconds, then 48°C for 45 seconds, then 72°C for 120 seconds; followed by a final extension at 72°C for 7 minutes. The forward and reverse primers used were based on human CD154 cDNA sequences outside the open reading frame in the 5' and 3' untranslated regions, respectively, so that the open reading frame in the PCR product contained only feline sequences. The sequence of the forward
10 primer was 5'GAAGATACCA TTTCAACTTT AACACAGC 3' SEQ ID NO:132, and that of the reverse primer was 5' TGCTGTATTG TGAAGACTCC CAGC 3' SEQ ID NO:133. PCR products were cloned into the TA cloning vector (available from Invitrogen Corporation, Carlsbad, CA), and the resulting clones were sequenced using an ABI Prism™ Model 377 Automatic DNA Sequencer (available from PE Applied
15 Biosystems Inc.). DNA sequencing reactions were performed using Prism™ dRhodamine Terminator Cycle Sequencing Ready Reaction kits (available from PE Applied Biosystems Inc.).

The PCR product was sequenced and found to contain 885 nucleotides, and is denoted as nFeCD154₈₈₅. The nucleotide sequence of the coding strand of nFeCD154₈₈₅
20 is represented herein as SEQ ID NO:72, and its complement is denoted SEQ ID NO:74. Translation of the open reading frame in SEQ ID NO:72 suggests that nFeCD154₈₈₅ encodes a protein containing 260 amino acids, referred to herein as PFeCD154₂₆₀, the amino acid sequence of which is presented as SEQ ID NO:73, assuming an open reading frame in which the first codon spans from nucleotide 29 through nucleotide 31 of SEQ
25 ID NO:72, and the stop codon spans from nucleotide 809 through nucleotide 811 of SEQ ID NO:72. The encoded protein has a predicted molecular weight of 28.6 kDa for the precursor protein and 27.2 kDa for the mature protein. The coding region encoding PFeCD154₂₆₀, not including the termination codon, is presented herein as nFeCD154₇₈₀.

which has the nucleotide sequence SEQ ID NO:75 (the coding strand) and SEQ ID NO:76 (the complementary strand)

A putative signal/membrane anchor sequence coding region extends from nucleotide 29 through nucleotide 175 of SEQ ID NO:72. The proposed soluble feline
5 CD154 protein, denoted herein as PFeCD154₂₁₁, represented by SEQ ID NO:78, contains about 211 amino acids, extending from residue 50 through residue 260 of SEQ ID NO:73. The nucleotide sequence encoding PFeCD154₂₁₁, denoted herein as nFeCD154₆₃₃ which extends from nucleotide 176 through nucleotide 808 of SEQ ID NO:72, is represented herein by SEQ ID NO:77 (the coding strand) and SEQ ID NO: 79 (the complementary
10 strand).

Comparison of feline CD154 nucleotide and amino acid sequences with those of other species published in GenBank reveals that the feline CD154 nucleotide sequence SEQ ID NO:75 is 86%, 88% and 75% identical to the human, bovine and murine CD154 gene sequences, respectively (Genbank accession number L07414, Z48469 and X56453
15 respectively). At the amino acid sequence level, SEQ ID NO:73 is 81%, 82%, and 67% identical to the human, bovine and murine CD154 amino acid sequences, respectively. Hydrophobicity analysis of feline CD154 proteins results in a pattern similar to those of human, bovine and murine CD154 proteins. A putative N-glycosylation site was identified at position 239 in PFeCD154₂₆₀ that is conserved in the human, bovine and
20 murine amino acid sequences. Five cysteine residues are present in the feline CD154 protein sequence SEQ ID NO:73. Four of the five residues, located at positions 72, 84, 177 and 217 of PFeCD154₂₆₀, are conserved in all four species and are likely involved in disulfide bond formation. The cysteine residue located at position 193 of PFeCD154₂₆₀ is present in all but the murine sequence.

25 Example 5

This example describes the isolation and sequencing of certain canine IL-5 nucleic acid molecules and proteins of the present invention. This example also describes expression of canine IL-5 in a *Pichia* expression system.

A. Isolation and sequencing of canine IL-5 nucleic acid molecules and proteins

A canine IL-5 cDNA nucleic acid molecule encoding a canine IL-5 protein was isolated by PCR amplification from a canine PBMC cDNA library (prepared as described in Example 1) using PCR conditions as described in Example 4B and the following primers. Degenerate oligonucleotide primers were designed in accordance with conserved regions of human and cat IL-5 gene sequences available in GenBank: sense primer, 5' ATGCACTTTC TTTGCC 3', denoted herein as SEQ ID NO:134; antisense primer 1, 5' CTGGAGGAAA AKACTTCRAT GATTCTGATA TCTGAAATAT AT 3', denoted herein as SEQ ID NO:135; and antisense primer 2, 5' CTGACYCTTK STTGGSCCTC ATTCTCA 3', denoted herein as SEQ ID NO:136, where K was G or T, R was either A or G, S was either G or C, and Y was either T or C.

An about 610-nucleotide canine IL-5 nucleic acid molecule, denoted nCaIL-5₆₁₀, was obtained using primers having SEQ ID NO:134 and SEQ ID NO:135, respectively. The sequence of the coding strand of nCaIL-5₆₁₀ is represented herein as SEQ ID NO:80. The reverse complement of SEQ ID NO:80 is referred to herein as SEQ ID NO:82. Translation of SEQ ID NO:80 suggests that nucleic acid molecule nCaIL-5₆₁₀ encodes an IL-5 protein of 134 amino acids, denoted herein as PCaIL-5₁₃₄, the amino acid sequence of which is presented in SEQ ID NO:81, assuming an open reading frame having an initiation codon spanning from nucleotide 29 through nucleotide 31 of SEQ ID NO:80 and a stop codon spanning from nucleotide 431 through nucleotide 433 of SEQ ID NO:80. The coding region encoding PCaIL-5₁₃₄, not including the termination codon, is presented herein as nCaIL-5₄₀₂, which has the nucleotide sequence SEQ ID NO:83 (the coding strand) and SEQ ID NO:84 (the complementary strand).

An about 488-nucleotide fragment, denoted herein as nCaIL-5₄₈₈, isolated by PCR with primers having SEQ ID NO:134 and SEQ ID NO:136, respectively, corresponds to nucleotide 1 through nucleotide 488 of nCaIL-5₆₁₀.

A putative signal sequence coding region extends from nucleotide 29 through nucleotide 85 of SEQ ID NO:80. The proposed mature protein, denoted herein as PCaIL-5₁₁₅, represented by SEQ ID NO:86, contains about 115 amino acids, extending from residue 20 through residue 134 of SEQ ID NO:81. The nucleotide sequence

encoding PCaIL-5₁₁₅, which extends from nucleotide 86 through nucleotide 430 of SEQ ID NO:80, is denoted herein as nucleic acid molecule nCaIL-5₃₄₅, represented by SEQ ID NO:85 (coding strand) and SEQ ID NO:87 (the complement strand).

Sequence analysis was performed with DNAsis™ using the alignment settings of: gap penalty set at 5; number of top diagonals set at 5; fixed gap penalty set at 10; k-tuple set at 2; window size set at 5 and floating gap penalty set at 10. At the amino acid level, PCaIL-5₁₃₄ shared 82.8% and 57.4% identity with feline and human IL-5 proteins, respectively (Padrid et al., *Am. J. Vet. Res.*, vol. 59, pp. 1263-1269, 1998; Azuma et al., *Nucleic Acids Res.*, vol. 14, pp. 9149-9158, 1986). At the nucleotide level, nCaIL-5₆₁₀ shared 81.7% and 75% identity with the cDNA sequences of the feline and human IL-5, respectively.

B. Expression of canine IL-5 in *Pichia*

This example describes the expression in *Pichia* of a canine IL-5 cDNA fragment, namely a canine IL-5 nucleic acid molecule denoted nCaIL-5₃₄₈, the coding strand of which consists of nucleotides 86-433 of SEQ ID NO:80, and as such, encodes a predicted mature canine IL-5 protein having SEQ ID NO:86. Nucleic acid molecule nCaIL-5₃₄₈, was PCR amplified from nCaIL-5₆₁₀ using sense primer 5' GGGCTCGAGA AAAGATTTGC TGTAGAAAAT CCCATG 3' denoted herein as SEQ ID NO:137, with nucleotides 16-36 corresponding to nucleotides 86-106 of SEQ ID NO:80; and antisense primer 5' CCCGCGGCCG CTCAACTTTC CGGTGTCCAC TC 3', denoted herein as SEQ ID NO:138, with nucleotides 12-32 corresponding to the reverse complement of nucleotides 413-433 of SEQ ID NO:80. To facilitate cloning, an *Xho*I site (shown in bold) was added to the sense primer and a *Not*I site (shown in bold) was added to the antisense primer. The PCR-amplified fragment was digested with restriction endonucleases *Xho*I and *Not*I, gel purified and ligated into pPICZαA plasmid vector, available from Invitrogen, that had been digested by *Xho*I and *Not*I and gel purified, to produce recombinant molecule pPICZαA-nCaIL-5₃₄₈. The insert in the recombinant molecule was verified by DNA sequencing. The recombinant molecule was used to transform *Pichia pastoris* strain X-33 by electroporation to produce recombinant cell *Pichia*-pPICZαA-nCaIL-5₃₄₈. Recombinant cell *Pichia*-pPICZαA-nCaIL-5₃₄₈ was cultured using techniques known to those skilled in the art and IL-5 expression was

induced with methanol. The supernatant was recovered and submitted to SDS-PAGE. Silver staining of the resultant gel indicated a band of about 18 kDa only seen in the supernatant of *Pichia* transformed with recombinant molecule pPICZ α A-nCaIL-5₃₄₈.

Example 6

5 This example describes the isolation and sequencing of certain canine IL-13 nucleic acid molecules and proteins of the present invention. This example also describes expression of canine IL-13 in *E. coli*.

A. Isolation and sequencing of canine IL-13 nucleic acid molecules and proteins

10 A canine IL-13 cDNA nucleic acid molecule encoding a canine IL-13 protein was isolated by PCR amplification from a canine PBMC cDNA library (prepared as described in Example 1) using the following primers and PCR conditions: Degenerate oligonucleotide primers were designed in accordance with conserved regions of human and cat IL-5 gene sequences available in GenBank: sense primer, 5' GTCMTKGCTC
15 TYRCTTGCCT TGG 3', denoted herein as SEQ ID NO:139; antisense primer 1, 5' AASTGGGCY ACYTCGATTT TGG 3', denoted herein as SEQ ID NO:140; antisense primer 2, 5' GTGATGTTGM YCAGCTCCTC 3', denoted herein as SEQ ID NO:141, where M was either A or C, K was G or T, R was either A or G, S was either G or C, and Y was either T or C. PCR conditions used were as follows: One initial
20 denaturation step at 95°C for 3 minutes; then 38 cycles of the following: 94°C for 30 seconds, 51.8°C for 45 seconds, then 72°C for 105 seconds; then a final extension at 72°C for 5 minutes.

An about 272-nucleotide canine IL-13 nucleic acid molecule, denoted nCaIL-13₂₇₂ and having a coding strand represented by SEQ ID NO:89, was PCR amplified
25 using primers having nucleic acid sequences of SEQ ID NO:139 and SEQ ID NO:140, respectively. An about 166-nucleotide canine IL-13 nucleic acid molecule, denoted nCaIL-13₁₆₆ and having a coding strand represented by SEQ ID NO:88, was isolated using primers having nucleic acid sequences of SEQ ID NO:142 (see Example 2B) and SEQ ID NO:141, respectively. Nucleic acid molecules nCaIL-13₂₇₂ and nCaIL-13₂₇₂
30 form a overlapping composite fragment of 383 nucleotides, denoted nCaIL-13₃₈₃. Two canine IL-13 specific primers (i.e., sense primer, 5' A⁺TGGCGCTCT GGTTGACTGT

3', denoted herein as SEQ ID NO:143; and antisense primer, 5' GGCTTTTGAG AGCACAGTGC 3', denoted herein as SEQ ID NO:144) were derived from nCaIL-13₃₈₃ and were used to isolate a 278-nucleotide fragment, denoted nCaIL-13₂₇₈ and having a coding strand represented by SEQ ID NO:90. Nucleic acid molecule nCaIL-13₂₇₈ was
5 radiolabeled and used to screen the canine PBMC cDNA library under the following hybridization conditions: hybridization took place in 6X SSC, 5X Denhardt's solution, 0.5% SDS, 100 µg/ml single stranded DNA, 100 µg/ml tRNA, for 36 hours at 60°C; the final wash solution was 0.1% SDS, 0.125X SSC at 60°C for 30 minutes. Two clones were selected, namely clone 80 and clone 78.

10 Sequence analysis of Clone 80 indicated that the clone includes an about 1302-nucleotide canine IL-13 nucleic acid molecule referred to herein as nCaIL-13₁₃₀₂, the coding strand of which was shown to have nucleic acid sequence SEQ ID NO:91. The reverse complement of SEQ ID NO:91 is referred to herein as SEQ ID NO:93. Translation of SEQ ID NO:91 suggests that nucleic acid molecule nCaIL-13₁₃₀₂
15 encodes an IL-13 protein of 131 amino acids, denoted herein as PCaIL-13₁₃₁, the amino acid sequence of which is presented in SEQ ID NO:92, assuming an open reading frame having an initiation codon spanning from nucleotide 52 through nucleotide 54 of SEQ ID NO:91 and a stop codon spanning from nucleotide 445 through nucleotide 447 of SEQ ID NO:91. The coding region encoding PCaIL-13₁₃₁, not including the termination
20 codon, is presented herein as nCaIL-13₃₉₃, which has the nucleotide sequence SEQ ID NO:94 (the coding strand) and SEQ ID NO:95 (the complementary strand).

A putative signal sequence coding region extends from nucleotide 52 to nucleotide 111 of SEQ ID NO:91. The proposed mature protein, denoted herein as PCaIL-13₁₁₁, represented by SEQ ID NO:97, contains 111 amino acids, extending from
25 residue 21 through residue 131 of SEQ ID NO:91. The nucleotide sequence encoding PCaIL-13₁₁₁, which extends from nucleotide 112 through nucleotide 444 of SEQ ID NO:91, is denoted herein as nucleic acid molecule nCaIL-13₃₃₃, represented by SEQ ID NO:96 (coding strand) and SEQ ID NO:98 (the complement strand).

Sequence analysis of Clone 78 indicated that the clone includes an about 1269-nucleotide canine IL-13 nucleic acid molecule referred to herein as nCaIL-13₁₂₆₉, the
30 coding strand of which was shown to have nucleic acid sequence SEQ ID NO:99. The

reverse complement of SEQ ID NO:99 is referred to herein as SEQ ID NO:101.

Translation of SEQ ID NO:99 suggests that nucleic acid molecule nCaIL-13₁₂₆₉ encodes an IL-13 protein of 130 amino acids, denoted herein as PCaIL-13₁₃₀, the amino acid sequence of which is presented in SEQ ID NO:100, assuming an open reading frame
5 having an initiation codon spanning from nucleotide 57 through nucleotide 59 of SEQ ID NO:99 and a stop codon spanning from nucleotide 447 through nucleotide 449 of SEQ ID NO:99. The coding region encoding PCaIL-13₁₃₀, not including the termination codon, is represented herein as nCaIL-13₃₉₀, which has the nucleotide sequence SEQ ID NO:102 (the coding strand) and SEQ ID NO:103 (the complementary strand). PCaIL-
10 13₁₃₀ is missing one amino acid compared to PCaIL-13₁₃₃, namely amino acid position Q97 of PCaIL-13₁₃₃.

A putative signal sequence coding region extends from nucleotide 57 to nucleotide 116 of SEQ ID NO:99. The proposed mature protein, denoted herein as PCaIL-13₁₁₀, represented by SEQ ID NO:105, contains 110 amino acids, extending from
15 residue 21 through residue 130 of SEQ ID NO:100. The nucleotide sequence encoding PCaIL-13₁₁₀, which extends from nucleotide 117 through nucleotide 446 of SEQ ID NO:99, is denoted herein as nucleic acid molecule nCaIL-13₃₃₀, represented by SEQ ID NO:104 (coding strand) and SEQ ID NO:106 (the complement strand).

Sequence analysis was performed with DNAsis™ using the alignment settings
20 of: gap penalty set at 5; number of top diagonals set at 5; fixed gap penalty set at 10; k-tuple set at 2; window size set at 5 and floating gap penalty set at 10. At the amino acid level, PCaIL-13₁₃₁ shared 61.7%, 39.6%, 36.6% identity with the IL-13 proteins of human, mouse, and rat (Brown et al., *J. Immunol.*, vol. 142, pp. 679-687, 1989; Lakkis et al., *Biochem. Biophys. Res. Commun.*, Vol. 197, pp. 612-618, 1993; McKenzie et al.,
25 *Proc. Natl Acad. Sci. USA*, vol. 90, pp. 3735-3739, 1993; Minty et al., *Nature*, vol. 362, pp. 248-250, 1993), respectively. At the nucleotide level, nCaIL-13₁₃₀₂ shared 56.0%, 57.1%, and 45.9% identity with the sequences of human, rat, and mouse IL-13 cDNAs, respectively.

B. Expression of canine IL-13 in *E. coli*

30 This example describes the expression in *E. coli* of a canine IL-13 cDNA fragment, namely a canine IL-13 nucleic acid molecule denoted nCaIL-13₃₃₆, the coding

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strand of which consists of nucleotides 112-447 of SEQ ID NO:91, and as such, encodes a predicted mature canine IL-13 protein having SEQ ID NO:97. Nucleic acid molecule nCaIL-13₃₃₆ was PCR amplified from nCaIL-13₁₃₀₂ using sense primer 5' CCCCATATGA GCCCTGTGAC TCCCTCCCC 3' denoted herein as SEQ ID:145, with nucleotides 10-29 corresponding to nucleotides 112-1131 of SEQ ID NO:91; and antisense primer 5' GGGGAATTCT CATCTGAAAT TTCCATGGCG 3', denoted herein as SEQ ID NO:146, with nucleotides 10-30 corresponding to the reverse complement of nucleotides 427-447 of SEQ ID NO:91. To facilitate cloning, an *NdeI* site (shown in bold) was added to the sense primer and an *EcoRI* site (shown in bold) was added to the antisense primer. The resulting PCR fragment was digested with restriction endonucleases *NdeI* and *EcoRI*, gel purified and ligated into λ cro plasmid vector, the production of which is described in U.S. Patent No. 5,569,603 by Tripp et al., issued October 29, 1996, that had been digested by *NdeI* and *EcoRI* and gel purified to produce recombinant molecule p λ cro-nCaIL-13₃₃₆. The insert in the recombinant molecule was verified by DNA sequencing. Recombinant molecule p λ cro-nCaIL-13₃₃₆ was used to transform *E. coli* strain HCE101 (BL21), thereby producing BL21-p λ cro-nCaIL-13₃₃₆. PCaIL-13₁₁₁ was produced under conditions as described in U.S. Patent No. 5,569,603, *ibid.*, protein expression being induced by switching the fermentation temperature from 32°C to 42°C. SDS-PAGE and Commassie blue staining analysis indicated that a band of about 11 kD was only produced by induced BL21-p λ cro-nCaIL-13₃₃₆ recombinant cells. The 11-kD band showed a positive reaction with a rabbit polyclonal antibody against human IL-13 (available from PeproTech Inc, Rocky Hill, NJ), indicating expression of canine IL-13 in *E. coli*.

Example 7

25 This example describes the isolation and sequencing of feline interferon alpha nucleic acid molecules and proteins of the present invention.

Feline IFN-alpha nucleic acid molecules were PCR amplified from a feline cDNA library as follows. Total RNA was isolated from cat (kitten) mesenteric lymph node cells stimulated with PMA (phorbol myristate acetate) for 48 hours using Tri Reagent™ (available from Molecular Research Center, Cincinnati, Ohio). cDNA was made from the RNA using the cDNA synthesis kit containing Ready to Go -You Prime

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First-Strand Beads™ (available from Amersham Pharmacia Biotech, Piscataway, NJ). An aliquot of this cDNA was used as a template to isolate a feline IFN-alpha nucleic acid molecule by PCR amplification using Amplitaq DNA polymerase™ (available from PE Applied Biosystems Inc, Foster City, CA) and the following primers and

5 conditions. The sequence of the forward primer was 5' ATGGCGCTGC CCTCTTCCTT CTTG 3' (SEQ ID NO:143), and that of the reverse primer was 5' TCATTTCTCG CTCCTTAATC TTTTCTGC 3' (SEQ ID NO:148). The following PCR protocol was used: one initial denaturation step at 95°C for 5 minutes; then 43 cycles of the following: 94°C for 45 seconds, then 47°C for 45 seconds, then 72°C for 120 seconds;

10 followed by a final extension at 72°C for 7 minutes. PCR products were cloned into the TA cloning vector (available from Invitrogen Corporation) and the clones were sequenced using an ABI Prism™ Model 377 Automatic DNA Sequencer (available from PE Applied Biosystems Inc.). DNA sequencing reactions were performed using Prism™ dRhodamine Terminator Cycle Sequencing Ready Reaction kits (available from

15 PE Applied Biosystems Inc.).

Two PCR products were generated and sequenced. Both contained 570 nucleotides (including the termination codons), and are distinguished as Clone #2 and Clone #3 as there were differences in the sequences of the clones.

Clone #2 includes a feline IFN-alpha nucleic acid molecule that is represented

20 herein as nFeIFN α_{567a} , the coding strand of which was shown to have a nucleic acid sequence denoted herein as SEQ ID NO:107. The complement of SEQ ID NO:107 is represented herein by SEQ ID NO:109. Translation of SEQ ID NO:107 suggests that nFeIFN α_{567a} encodes a protein containing 189 amino acids, referred to herein as PFeIFN α_{189a} , with an amino acid sequence denoted SEQ ID NO:108. The open reading

25 frame of SEQ ID NO:107 is assumed to be the following: the first codon spans from nucleotide 1 through nucleotide 3 and the last codon before the stop codon spans from nucleotide 565 to nucleotide 567 of SEQ ID NO:107. The encoded protein has a predicted molecular weight of 21 kDa. The putative signal peptide cleavage site occurs between amino acid positions 23 and 24, based on homology with the human and canine

30 interferon-alpha proteins. The proposed mature protein (i.e. feline IFN α protein from which the signal sequence has been cleaved), denoted herein as PFeIFN α_{166a} , contains

about 166 amino acids, extending from residue 24 to residue 166 of SEQ ID NO:108; the amino acid sequence is denoted herein as SEQ ID NO:114. The nucleic acid molecule encoding PFeIFN α_{166a} is denoted herein as nFeIFN α_{498a} , which is represented by SEQ ID NO:113, with a complementary sequence represented by SEQ ID NO:115. A putative N-glycosylation site and an interferon alpha-beta-delta family signature motif are present at amino acid positions 102 and 145, respectively, of PFeIFN α_{189a} .

Clone #3 includes a feline IFN-alpha nucleic acid molecule that is represented herein as nFeIFN α_{567b} , the coding strand of which was shown to have a nucleic acid sequence denoted herein as SEQ ID NO:110. The complement of SEQ ID NO:110 is represented herein by SEQ ID NO:112. Translation of SEQ ID NO:110 suggests that nFeIFN α_{567b} encodes a protein containing 189 amino acids, referred to herein as PFeIFN α_{189b} , with an amino acid sequence denoted SEQ ID NO:111. The open reading frame of SEQ ID NO:110 is assumed to be the following: the first codon spans from nucleotide 1 through nucleotide 3 and the last codon before the stop codon spans from nucleotide 565 through nucleotide 567 of SEQ ID NO:110. The encoded protein has a predicted molecular weight of 21 kDa. The putative signal peptide cleavage site occurs between amino acid positions 23 and 24, based on homology with the human and canine interferon-alpha proteins. The proposed mature protein (i.e. feline IFN α protein from which the signal sequence has been cleaved), denoted herein as PFeIFN α_{166b} , contains about 166 amino acids, extending from residue 24 to residue 166 of SEQ ID NO:111; the amino acid sequence is denoted herein as SEQ ID NO:117. The nucleic acid molecule encoding PFeIFN α_{166b} is denoted herein as nFeIFN α_{498b} , which is represented by SEQ ID NO:116, with a complementary sequence represented by SEQ ID NO:118. A putative N-glycosylation site and an interferon alpha-beta-delta family signature motif are present at amino acid positions 102 and 145, respectively, of PFeIFN α_{189b} .

The differences between the proteins encoded by SEQ ID NO:107 and SEQ ID NO:110 are detailed as follows: The amino acid residues at position 56 in SEQ ID NO:108 (i.e., the protein encoded by SEQ ID NO:107) and at position 56 in SEQ ID NO:111 (i.e., the protein encoded by SEQ ID NO:110) are both arginines, although the corresponding codons in SEQ ID NO:107 and SEQ ID NO:110 are AGA and AGG, respectively. The amino acid residues at position 74 in SEQ ID NO:108 and at position

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74 in SEQ ID NO:111 are both alanines, although the corresponding codons in SEQ ID NO:107 and SEQ ID NO:110 are GCC and GCT, respectively. The amino acid residue at position 86 in SEQ ID NO:108 is lysine, encoded by AAG in SEQ ID NO:107, whereas the amino acid residue at position 86 in SEQ ID NO:111 is glutamic acid, encoded by GAG in SEQ ID NO:110. The amino acid residue at position 125 in SEQ ID NO:108 is methionine, encoded by CTG in SEQ ID NO:107, whereas the amino acid residue at position 125 in SEQ ID NO:111 is valine, encoded by GTG in SEQ ID NO:110. The amino acid residue at position 141 in SEQ ID NO:108 is isovaline, encoded by ATC in SEQ ID NO:107, whereas the amino acid residue at position 141 in SEQ ID NO:111 is leucine, encoded by CTC in SEQ ID NO:110.

Feline IFN-alpha proteins of the present invention PFeIFN α_{189a} and PfeIFN α_{189b} are five amino acids shorter than the GenBank entry for feline IFN-alpha, accession # E02521. In addition, there are 3 non-conservative and 2 conservative changes at the amino acid level between this GenBank entry and SEQ ID NO:108 (PFeIFN α_{189a}) as well as 4 non-conservative and 3 conservative changes at the amino acid level between this GenBank entry and SEQ ID NO:111 (PfeIFN α_{189b}). The lengths of SEQ ID NO:108 and SEQ ID NO:111, when compared with those of IFN-alpha proteins of other species, are two amino acids longer than published canine interferon-alpha subtype 1, 2 and 3 sequences, two amino acids longer than published human interferon-alpha type 1,B,D, F, and J sequences, three amino acids longer than the published human interferon-alpha sequence type A sequence and two amino acids longer than published murine interferon-alpha type B, 8, 7, 11, and 19 sequences.

Example 8

This example describes the isolation and sequencing of feline granulocyte-macrophage colony-stimulating factor (GMCSF) nucleic acid molecules and proteins of the present invention. This example also describes expression of a feline GMCSF protein of the present invention.

Nucleic acid molecules encoding feline GMCSF were isolated as follows. A cDNA library was prepared from feline PBMCs stimulated with Con A for 12 hours, as previously described in Example 2. An aliquot of this library was used as a template to amplify feline GMCSF nucleic acid molecules by PCR using Amr'itaq DNA

polymerase[™] (PE Applied Biosystems Inc, Foster City, CA) and the following primers and conditions. The sequence of the forward primer was 5'CAGGGATCCA CCATGTGGCT GCAGAACCTG CTTTTC 3' (SEQ ID NO:149), and that of the reverse primer was 5' TTACTTCTGG TCTGGTCCCC AGCAGTCAAA GGGGTTGTTA AACAGAAAAT 3' (SEQ ID NO:150). The following PCR protocol was used: one initial denaturation step at 95°C for 5 minutes; then 35 cycles of the following: 94°C for 30 seconds, then 50°C for 30 seconds, then 72°C for 90 seconds; followed by a final extension at 72°C for 7 minutes. PCR products were cloned into the CMV-Intron A vector and the clones were sequenced as described in Example 7.

10 A PCR product was isolated, referred to herein as nFeGMCSF₄₄₄, the coding strand of which is represented herein as SEQ ID NO:119, and its complement is denoted SEQ ID NO:121. Translation of the open reading frame in SEQ ID NO:119 suggests that nucleic acid molecule nFeGMCSF₄₄₄ encodes a protein containing 144 amino acids, referred to herein as PFeGMCSF₁₄₄, with an amino acid sequence denoted SEQ ID
15 NO:120, assuming an open reading frame in which the first codon spans from nucleotide 10 through nucleotide 12 of SEQ ID NO:119, and the stop codon spans from nucleotide 442 through nucleotide 444 of SEQ ID NO:121. The encoded protein has a predicted molecular weight of 16 kDa. The coding region encoding PFeGMCSF₁₄₄ is presented herein as nFeGMCSF₄₃₂ which has the nucleotide sequence SEQ ID NO:122 (the coding
20 strand) and SEQ ID NO:123 (the complementary strand). A putative signal peptide cleavage site is between amino acid positions 17 and 18, based on homology with human, mouse and ovine GMCSF proteins. The nucleic acid molecule encoding the proposed mature protein is denoted as nFeGMCSF₃₈₁ and has a nucleotide sequence represented herein as SEQ ID NO:124 and a complementary sequence represented
25 herein as SEQ ID NO:126. The amino acid sequence of the putative mature protein, referred to herein as PFeGMCSF₁₂₇, has an amino acid sequence represented herein as SEQ ID NO:125. The number of amino acids in the feline GMCSF protein is the same compared to human, porcine, ovine and canine GMCSF proteins. The feline GMCSF protein is one amino acid longer than bovine GMCSF and three amino acid longer than
30 murine GMCSF.

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The deduced amino acid sequence of the full-length feline GMCSF protein of the present invention has four non-conservative changes and one conservative change compared to a GenBank entry for feline GMCSF (accession # AF053007). Amino acids asparagine, methionine, threonine, and lysine at positions 10, 36, 56 and 126 of the
5 GenBank entry have been changed to glycine, isoleucine, alanine and asparagine, respectively, in PFeGMCSF₁₄₄. PFeGMCSF₁₄₄, containing the above-noted amino acid substitutions, appears to have GMCSF activity, as demonstrated by an experiment in which supernatant collected from Chinese Hamster Ovary (CHO) cells that were transiently transfected with a recombinant molecule encoding a feline GMCSF protein of
10 the present invention was able to induce proliferation of TF-1 cells.

While various embodiments of the present invention have been described in detail, it is apparent that modifications and adaptations of those embodiments will occur to those skilled in the art. It is to be expressly understood, however, that such modifications and adaptations are within the scope of the present invention, as set forth
15 in the following claims.

What is claimed is:

1. An isolated nucleic acid molecule selected from the group consisting of:
 - (a) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:19, and SEQ ID NO:21 or a homolog thereof, wherein said homolog has an at least 50 contiguous nucleotide region identical in sequence to a 50 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:19, and SEQ ID NO:21;
 - 10 (b) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:36, and SEQ ID NO:37, or a homolog thereof, 15 wherein said homolog has an at least 40 contiguous nucleotide region identical in sequence to a 40 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:36, and SEQ ID NO:37;
 - 20 (c) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, and SEQ ID NO:50, or a homolog thereof, wherein said homolog has an at least 30 contiguous 25 nucleotide region identical in sequence to a 30 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, and SEQ ID NO:50;
 - (d) an isolated nucleic acid molecule comprising a nucleic acid 30 sequence selected from the group consisting of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, and SEQ ID NO:59, or a

homolog thereof, wherein said homolog has an at least 40 contiguous nucleotide region identical in sequence to a 40 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, and SEQ ID NO:59;

5 (e) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:60 and SEQ ID NO:62, or a homolog thereof, wherein said homolog has an at least 30 contiguous nucleotide region identical in sequence to a 30 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:60 and SEQ ID NO:62;

10 (f) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69 and SEQ ID NO:71, or a homolog thereof, wherein said homolog has an at least 45 contiguous nucleotide region identical in sequence to a 45 contiguous nucleotide region of a nucleic acid sequence
15 selected from the group consisting of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69 and SEQ ID NO:71;

(g) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, and SEQ ID NO:79, or a homolog thereof,
20 wherein said homolog has an at least 35 contiguous nucleotide region identical in sequence to a 35 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, and SEQ ID NO:79;

(h) an isolated nucleic acid molecule comprising a nucleic acid
25 sequence selected from the group consisting of SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, and SEQ ID NO:87, or a homolog thereof, wherein said homolog has an at least 45 contiguous nucleotide region identical in sequence to a 45 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID
30 NO:84, SEQ ID NO:85, and SEQ ID NO:87;

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(i) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, and SEQ ID NO:106, or a homolog thereof, wherein said homolog has an at least 15 contiguous nucleotide region identical in sequence to a 15 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, and SEQ ID NO:106;

(j) an isolated nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:116, and SEQ ID NO:118; and

(k) an isolated nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, and SEQ ID NO:126.

2. An isolated nucleic acid molecule selected from the group consisting of:

(a) a nucleic acid molecule having a nucleic acid sequence that is at least about 92 percent identical to a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:19, and SEQ ID NO:21;

(b) a nucleic acid molecule having a nucleic acid sequence that is at least about 75 percent identical to a nucleic acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:36, and SEQ ID NO:37;

(c) a nucleic acid molecule having a nucleic acid sequence that is at least about 75 percent identical to a nucleic acid sequence selected from the group

consisting of SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, and SEQ ID NO:50;

(d) a nucleic acid molecule having a nucleic acid sequence that is at least about 70 percent identical to a nucleic acid sequence selected from the group
5 consisting of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, and SEQ ID NO:59;

(e) a nucleic acid molecule having a nucleic acid sequence that is at least about 70 percent identical to a nucleic acid sequence selected from the group consisting of SEQ ID NO:60 and SEQ ID NO:62;

10 (f) a nucleic acid molecule having a nucleic acid sequence that is at least about 85 percent identical to a nucleic acid sequence selected from the group consisting of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, and SEQ ID NO:71;

(g) a nucleic acid molecule having a nucleic acid sequence that is at least about 91 percent identical to a nucleic acid sequence selected from the group
15 consisting of SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, and SEQ ID NO:79;

(h) a nucleic acid molecule having a nucleic acid sequence that is at least about 90 percent identical to a nucleic acid sequence selected from the group
20 consisting of SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, and SEQ ID NO:87;

(i) a nucleic acid molecule having a nucleic acid sequence that is at least about 65 percent identical to a nucleic acid sequence selected from the group consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID
25 NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, and SEQ ID NO:106;

(j) a nucleic acid molecule having a nucleic acid sequence that is selected from the group consisting of SEQ ID NO:107, SEQ ID NO:109, SEQ ID
30 NO:110, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:116, and SEQ ID NO:118; and

(k) a nucleic acid molecule having a nucleic acid sequence that is selected from the group consisting of SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, and SEQ ID NO:126.

3. An isolated nucleic acid molecule selected from the group consisting of:

- 5 (a) a nucleic acid molecule having a nucleic acid sequence encoding an IL-4 protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 85 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:20 and (ii) a protein comprising a fragment of at least 20 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:20;
- 10 (b) a nucleic acid molecule having a nucleic acid sequence encoding a Flt-3 ligand protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 75 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, and SEQ ID NO:34, and (ii) a protein comprising a fragment of at least 25 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, and SEQ ID NO:34;
- 15 (c) a nucleic acid molecule having a nucleic acid sequence encoding a Flt-3 ligand protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 75 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:44 and SEQ ID NO:49 and (ii) a protein comprising a fragment of at least 25 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:44 and SEQ ID NO:49;
- 20 (d) a nucleic acid molecule having a nucleic acid sequence encoding a CD40 protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 70 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:53 and SEQ ID NO:58 and (ii) a protein comprising a fragment of at least 30 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:53 and SEQ ID NO:58;
- 25 (e) a nucleic acid molecule having a nucleic acid sequence encoding a CD40 protein selected from the group consisting of (i) a protein having an amino acid
- 30

sequence that is at least about 60 percent identical to an amino acid sequence comprising SEQ ID NO:61 and (ii) a protein comprising a fragment of at least 20 amino acids of an amino acid sequence comprising SEQ ID NO:61;

(f) a nucleic acid molecule having a nucleic acid sequence encoding a
5 CD154 protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 80 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:65 and SEQ ID NO:70, and (ii) a protein comprising a fragment of at least 35 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:65 and SEQ ID NO:70;

10 (g) a nucleic acid molecule having a nucleic acid sequence encoding a CD154 protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 85 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:73 and SEQ ID NO:78, and (ii) a protein comprising a fragment of at least 50 amino acids of an amino acid sequence selected
15 from the group consisting of SEQ ID NO:73 and SEQ ID NO:78;

(h) a nucleic acid molecule having a nucleic acid sequence encoding an IL-5 protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 85 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:81 and SEQ ID NO:86 and (ii) a protein
20 comprising a fragment of at least 20 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:81 and SEQ ID NO:86;

(i) a nucleic acid molecule having a nucleic acid sequence encoding an IL-13 protein selected from the group consisting of (i) a protein having an amino acid sequence that is at least about 70 percent identical to an amino acid sequence selected
25 from the group consisting of SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, and SEQ ID NO:105 and (ii) a protein comprising a fragment of at least 15 amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, and SEQ ID NO:105;

(j) a nucleic acid molecule having a nucleic acid sequence encoding
30 an interferon alpha protein having an amino acid sequence that is selected from the

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group consisting of amino acid sequence SEQ ID NO:108, SEQ ID NO:111, SEQ ID NO:114, and SEQ ID NO:117;

(k) a nucleic acid molecule having a nucleic acid sequence encoding a GMCSF protein having an amino acid sequence that is selected from the group
5 consisting of amino acid sequence SEQ ID NO:120, and SEQ ID NO:125, and

(l) a nucleic acid molecule comprising a complement of any of said nucleic acid molecules as set forth in (a), (b), (c), (d), (e), (f), (g), (h), (i), (j), or (k),

wherein said IL-4 protein elicits an immune response against an IL-4 protein selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:20 or is a protein
10 with interleukin-4 activity, said Flt-3 ligand protein elicits an immune response against a Flt-3 ligand protein selected from the group consisting of SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, SEQ ID NO:34, SEQ ID NO:44, and SEQ ID NO:49 or is a protein with Flt-3 ligand activity, said CD40 protein elicits an immune response against a CD40 protein selected from the group consisting of SEQ ID NO:53,
15 SEQ ID NO:58, and SEQ ID NO:61 or is a protein with CD40 activity, said CD154 protein elicits an immune response against a CD154 protein selected from the group consisting of SEQ ID NO:65, SEQ ID NO:70, SEQ ID NO:73, and SEQ ID NO:78 or is a protein with CD154 activity, said IL-5 protein elicits an immune response against a IL-5 protein selected from the group consisting of SEQ ID NO:81 and SEQ ID NO:86 or is
20 a protein with IL-5 activity, said IL-13 protein elicits an immune response against an IL-13 protein selected from the group consisting of SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, and SEQ ID NO:105 or is a protein with IL-13 activity, said interferon alpha protein elicits an immune response against an interferon alpha protein selected from the group consisting of SEQ ID NO:108, SEQ ID NO:111, SEQ ID NO:114, and SEQ ID
25 NO:117 or is a protein with interferon alpha activity, and said GMCSF protein elicits an immune response against a GMCSF protein selected from the group consisting of SEQ ID NO:120 and SEQ ID NO:125 or is a protein with GM-CSF activity.

4. An isolated protein selected from the group consisting of:

(a) (i) an isolated protein of at least about 20 amino acids in
30 length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 60 contiguous nucleotide region identical in sequence to a

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60 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:4, and SEQ ID NO:19; and

(ii) an isolated protein of at least about 20 amino acids in length, wherein said protein has an at least 20 contiguous amino acid region identical in sequence to a 20 contiguous amino acid region selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:20,

wherein said isolated protein elicits an immune response against a canine IL-4 protein or has IL-4 activity;

(b) (i) an isolated protein of at least about 20 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 60 contiguous nucleotide region identical in sequence to a 60 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:9, SEQ ID NO:22, SEQ ID NO:25, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:33, and SEQ ID NO:36; and

(ii) an isolated protein of at least about 20 amino acids in length, wherein said protein has an at least 20 contiguous amino acid region identical in sequence to a 20 contiguous amino acid region selected from the group consisting of SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, and SEQ ID NO:34,

wherein said isolated protein elicits an immune response against a canine Flt-3 ligand protein or has Flt-3 activity;

(c) (i) an isolated protein of at least about 20 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 60 contiguous nucleotide region identical in sequence to a 60 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:46, and SEQ ID NO:48; and

(ii) an isolated protein of at least about 20 amino acids in length, wherein said protein has an at least 20 contiguous amino acid region identical in sequence to a 20 contiguous amino acid region selected from the group consisting of SEQ ID NO:44 and SEQ ID NO:49,

wherein said isolated protein elicits an immune response against a feline Flt-3 ligand protein or has Flt-3 activity;

(d) (i) an isolated protein of at least about 30 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 90 contiguous nucleotide region identical in sequence to a
5 90 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:55, and SEQ ID NO:57; and

(ii) an isolated protein of at least about 30 amino acids in length, wherein said protein has an at least 30 contiguous amino acid region identical in
10 sequence to a 30 contiguous amino acid region selected from the group consisting of SEQ ID NO:53, and SEQ ID NO:58,

wherein said isolated protein elicits an immune response against a canine CD40 protein or has CD40 activity;

(e) (i) an isolated protein of at least about 20 amino acids in
15 length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 60 contiguous nucleotide region identical in sequence to a 60 contiguous nucleotide region of a nucleic acid sequence comprising SEQ ID NO:60; and

(ii) an isolated protein of at least about 20 amino acids in
20 length, wherein said protein has an at least 20 contiguous amino acid region identical in sequence to a 20 contiguous amino acid region comprising SEQ ID NO:61,

wherein said isolated protein elicits an immune response against a feline CD40 protein or has CD40 activity;

(f) (i) an isolated protein of at least about 35 amino acids in
25 length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 105 contiguous nucleotide region identical in sequence to a 105 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:67, and SEQ ID NO:69; and

(ii) an isolated protein of at least about 35 amino acids in
30 length, wherein said protein has an at least 35 contiguous amino acid region identical in

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sequence to a 35 contiguous amino acid region selected from the group consisting of SEQ ID NO:65 and SEQ ID NO:70,

wherein said isolated protein elicits an immune response against a canine CD154 protein or has CD154 activity;

5 (g) (i) an isolated protein of at least about 50 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 150 contiguous nucleotide region identical in sequence to a 150 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:72, SEQ ID NO:75, and SEQ ID NO:77; and

10 (ii) an isolated protein of at least about 50 amino acids in length, wherein said protein has an at least 50 contiguous amino acid region identical in sequence to a 50 contiguous amino acid region selected from the group consisting of SEQ ID NO:73 and SEQ ID NO:78,

wherein said isolated protein elicits an immune response against a feline CD154 protein or has CD154 activity;

15 (h) (i) an isolated protein of at least about 20 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 60 contiguous nucleotide region identical in sequence to a 60 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:80, SEQ ID NO:83, and SEQ ID NO:85; and

20 (ii) an isolated protein of at least about 20 amino acids in length, wherein said protein has an at least 20 contiguous amino acid region identical in sequence to a 20 contiguous amino acid region selected from the group consisting of SEQ ID NO:81 and SEQ ID NO:86,

25 wherein said isolated protein elicits an immune response against a canine IL-5 protein or has IL-5 activity;

(i) (i) an isolated protein of at least about 15 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 45 contiguous nucleotide region identical in sequence to a 45 contiguous nucleotide region of a nucleic acid sequence selected from the group

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consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:102, and SEQ ID NO:104; and

(ii) . an isolated protein of at least about 15 amino acids in length, wherein said protein has an at least 15 contiguous amino acid region identical in
5 sequence to a 15 contiguous amino acid region selected from the group consisting of SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, and SEQ ID NO:105,

wherein said isolated protein elicits an immune response against a canine IL-13 protein or has IL-13 activity;

(j) (i) an isolated protein encoded by a nucleic acid molecule
10 selected from the group consisting of SEQ ID NO:107, SEQ ID NO:110, SEQ ID NO:113, and SEQ ID NO:116, and

(ii) an isolated protein selected from the group consisting of SEQ ID NO:108, SEQ ID NO:111, SEQ ID NO:114, and SEQ ID NO:117,

wherein said isolated protein elicits an immune response against a feline
15 interferon alpha protein or has interferon alpha activity;

(k) (i) an isolated protein encoded by a nucleic acid molecule selected from the group consisting of SEQ ID NO:119, SEQ ID NO:122, and SEQ ID NO:124, and

(ii) an isolated protein selected from the group consisting of
20 SEQ ID NO:120 and SEQ ID NO:125,

wherein said isolated protein elicits an immune response against a feline GM-CSF or has GM-CSF activity.

5. An isolated protein selected from the group consisting of:

(a) a protein having an amino acid sequence that is at least about 85
25 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:20;

(b) a protein having an amino acid sequence that is at least about 75 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, and SEQ ID NO:34;

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(c) a protein having an amino acid sequence that is at least about 75 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:44 and SEQ ID NO:49;

(d) a protein having an amino acid sequence that is at least about 70 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:53 and SEQ ID NO:58;

(e) a protein having an amino acid sequence that is at least about 60 percent identical to an amino acid sequence comprising SEQ ID NO:61;

(f) a protein having an amino acid sequence that is at least about 80 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:65 and SEQ ID NO:70;

(g) a protein having an amino acid sequence that is at least about 85 percent identical to the amino acid sequence SEQ ID NO:73 and SEQ ID NO:78;

(h) a protein having an amino acid sequence that is at least about 85 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:81 and SEQ ID NO:86;

(i) a protein having an amino acid sequence that is at least about 70 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, and SEQ ID NO:105;

(j) a protein having an amino acid sequence selected from the group consisting of SEQ ID NO:108, SEQ ID NO:111, SEQ ID NO:114, and SEQ ID NO:117; and

(k) a protein having an amino acid sequence selected from the group consisting of SEQ ID NO:120, and SEQ ID NO:125.

6. A therapeutic composition that, when administered to an animal, regulates an immune response in said animal, said therapeutic composition comprising a therapeutic compound selected from the group consisting of:

a. an isolated protein comprising an immunoregulatory protein, wherein said protein is selected from the group consisting of

(a) (i) an isolated protein of at least about 20 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic

acid molecule has an at least 60 contiguous nucleotide region identical in sequence to a 60 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:4, SEQ ID NO:19; and

- (ii) an isolated protein of at least about 20 amino acids in length, wherein said protein has an at least 20 contiguous amino acid region identical in sequence to a 20 contiguous amino acid region selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:20,

wherein said isolated protein elicits an immune response against a canine IL-4 protein or has IL-4 activity;

- (b) (i) an isolated protein of at least about 20 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 60 contiguous nucleotide region identical in sequence to a 60 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:9, SEQ ID NO:22, SEQ ID NO:25, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:33, and SEQ ID NO:36; and

- (ii) an isolated protein of at least about 20 amino acids in length, wherein said protein has an at least 20 contiguous amino acid region identical in sequence to a 20 contiguous amino acid region selected from the group consisting of SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, and SEQ ID NO:34, wherein said isolated protein elicits an immune response against a canine Flt-3 ligand protein or has Flt-3 activity;

- (c) (i) an isolated protein of at least about 20 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 60 contiguous nucleotide region identical in sequence to a 60 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:46, and SEQ ID NO:48; and

- (ii) an isolated protein of at least about 20 amino acids in length, wherein said protein has an at least 20 contiguous amino acid region identical in sequence to a 20 contiguous amino acid region selected from the group consisting of SEQ ID NO:44 and SEQ ID NO:49,

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wherein said isolated protein elicits an immune response against a feline Flt-3 ligand protein or has Flt-3 activity;

(d) (i) an isolated protein of at least about 30 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 90 contiguous nucleotide region identical in sequence to a
5 90 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:55, and SEQ ID NO:57; and

(ii) an isolated protein of at least about 30 amino acids in length, wherein said protein has an at least 30 contiguous amino acid region identical in
10 sequence to a 30 contiguous amino acid region selected from the group consisting of SEQ ID NO:53, SEQ ID NO:58,

wherein said isolated protein elicits an immune response against a canine CD40 protein or has CD40 activity;

(e) (i) an isolated protein of at least about 20 amino acids in
15 length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 60 contiguous nucleotide region identical in sequence to a 60 contiguous nucleotide region of a nucleic acid sequence comprising SEQ ID NO:60; and

(ii) an isolated protein of at least about 20 amino acids in
20 length, wherein said protein has an at least 20 contiguous amino acid region identical in sequence to a 20 contiguous amino acid region comprising the amino acid sequence SEQ ID NO:61,

wherein said isolated protein elicits an immune response against a feline CD40 protein or has CD40 activity;

25 (f) (i) an isolated protein of at least about 35 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 105 contiguous nucleotide region identical in sequence to a 105 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:67, and SEQ ID NO:69; and

30 (ii) an isolated protein of at least about 35 amino acids in length, wherein said protein has an at least 35 contiguous amino acid region identical in

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sequence to a 35 contiguous amino acid region selected from the group consisting of SEQ ID NO:65 and SEQ ID NO:70,

wherein said isolated protein elicits an immune response against a canine CD154 protein or has CD154 activity;

5 (g) (i) an isolated protein of at least about 50 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 150 contiguous nucleotide region identical in sequence to a 150 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:72, SEQ ID NO:75, and SEQ ID NO:77; and

10 (ii) an isolated protein of at least about 50 amino acids in length, wherein said protein has an at least 50 contiguous amino acid region identical in sequence to a 50 contiguous amino acid region selected from the group consisting of SEQ ID NO:73 and SEQ ID NO:78,

wherein said isolated protein elicits an immune response against a feline CD154 protein or has CD154 activity;

(h) (i) an isolated protein of at least about 20 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 60 contiguous nucleotide region identical in sequence to a 60 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:80, SEQ ID NO:83, and SEQ ID NO:85; and

20 (ii) an isolated protein of at least about 20 amino acids in length, wherein said protein has an at least 20 contiguous amino acid region identical in sequence to a 20 contiguous amino acid region selected from the group consisting of SEQ ID NO:81 and SEQ ID NO:86,

25 wherein said isolated protein elicits an immune response against a canine IL-5 protein or has IL-5 activity;

(i) (i) an isolated protein of at least about 15 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 45 contiguous nucleotide region identical in sequence to a 45 contiguous nucleotide region of a nucleic acid sequence selected from the group

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consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:102, and SEQ ID NO:104; and

- (ii) an isolated protein of at least about 15 amino acids in length, wherein said protein has an at least 15 contiguous amino acid region identical in sequence to a 15 contiguous amino acid region selected from the group consisting of
- 5 SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, and SEQ ID NO:105,

wherein said isolated protein elicits an immune response against a canine IL-13 protein or has IL-13 activity;

- (j) (i) an isolated protein encoded by a nucleic acid molecule
- 10 selected from the group consisting of SEQ ID NO:107, SEQ ID NO:110, SEQ ID NO:113, and SEQ ID NO:116, and

(ii) an isolated protein selected from the group consisting of SEQ ID NO:108, SEQ ID NO:111, SEQ ID NO:114, and SEQ ID NO:117,

wherein said isolated protein elicits an immune response against a feline

15 interferon alpha protein or has interferon alpha activity;

- (k) (i) an isolated protein encoded by a nucleic acid molecule selected from the group consisting of SEQ ID NO:119, SEQ ID NO:122, and SEQ ID NO:124, and

(ii) an isolated protein selected from the group consisting of

20 SEQ ID NO:120 and SEQ ID NO:125,

wherein said isolated protein elicits an immune response against a feline GM-CSF or has GM-CSF activity;

- b. a mimotope of any of said immunoregulatory proteins;
- c. a multimeric form of any of said immunoregulatory proteins;
- 25 d. an isolated nucleic acid molecule selected from the group consisting of
- (a) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:19, SEQ ID NO:21 or a homolog thereof, wherein said homolog has an at least 50 contiguous nucleotide region identical in sequence to a
- 30 50 contiguous nucleotide region of a nucleic acid sequence selected from the group

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consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:19, SEQ ID NO:21;

(b) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:36, and SEQ ID NO:37, or a homolog thereof, wherein said homolog has an at least 40 contiguous nucleotide region identical in sequence to a 40 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:36, and SEQ ID NO:37,;

(c) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, and SEQ ID NO:50, or a homolog thereof, wherein said homolog has an at least 30 contiguous nucleotide region identical in sequence to a 30 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, and SEQ ID NO:50;

(d) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, and SEQ ID NO:59, or a homolog thereof, wherein said homolog has an at least 40 contiguous nucleotide region identical in sequence to a 40 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, and SEQ ID NO:59;

(e) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:60 and SEQ ID NO:62, or a homolog thereof, wherein said homolog has an at least 30 contiguous nucleotide region

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identical in sequence to a 30 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:60 and SEQ ID NO:62;

(f) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69 and SEQ ID NO:71, or a homolog thereof, wherein said homolog has an at least 45 contiguous nucleotide region identical in sequence to a 45 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69 and SEQ ID NO:71;

(g) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, and SEQ ID NO:79, or a homolog thereof, wherein said homolog has an at least 35 contiguous nucleotide region identical in sequence to a 35 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, and SEQ ID NO:79;

(h) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, and SEQ ID NO:87, or a homolog thereof, wherein said homolog has an at least 45 contiguous nucleotide region identical in sequence to a 45 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, and SEQ ID NO:87;

(i) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, and SEQ ID NO:106, or a homolog thereof, wherein said homolog has an at least 15 contiguous nucleotide region identical in sequence to a 15 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID

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NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, and SEQ ID NO:106;

(j) an isolated nucleic acid molecule having a nucleic acid sequence
5 selected from the group consisting of SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:116, and SEQ ID NO:118; and

(k) an isolated nucleic acid molecule having a nucleic acid sequence
selected from the group consisting of SEQ ID NO:119, SEQ ID NO:121, SEQ ID
10 NO:122, SEQ ID NO:123, SEQ ID NO:124, and SEQ ID NO:126;

e. an antibody that selectively binds to any of said immunoregulatory proteins; and

f. an inhibitor of a immunoregulatory protein activity identified by its ability to inhibit the activity of any of said immunoregulatory proteins.

15 7. A method to regulate an immune response in an animal comprising administering to the animal a therapeutic composition comprising a therapeutic compound selected from the group consisting of:

(a) (i) an isolated protein of at least about 20 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 60 contiguous nucleotide region identical in sequence to a
20 60 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:4, SEQ ID NO:19; and

(ii) an isolated protein of at least about 20 amino acids in length, wherein said protein has an at least 20 contiguous amino acid region identical in
25 sequence to a 20 contiguous amino acid region selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:20,

wherein said isolated protein elicits an immune response against a canine IL-4 protein or has IL-4 activity;

(b) (i) an isolated protein of at least about 20 amino acids in
30 length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 60 contiguous nucleotide region identical in sequence to a

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- 60 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:9, SEQ ID NO:22, SEQ ID NO:25, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:33, and SEQ ID NO:36; and
- (ii) an isolated protein of at least about 20 amino acids in
5 length, wherein said protein has an at least 20 contiguous amino acid region identical in sequence to a 20 contiguous amino acid region selected from the group consisting of SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, and SEQ ID NO:34, wherein said isolated protein elicits an immune response against a canine Flt-3 ligand protein or has Flt-3 activity;
- 10 (c) (i) an isolated protein of at least about 20 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 60 contiguous nucleotide region identical in sequence to a 60 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:46, and SEQ
15 ID NO:48; and
- (ii) an isolated protein of at least about 20 amino acids in length, wherein said protein has an at least 20 contiguous amino acid region identical in sequence to a 20 contiguous amino acid region selected from the group consisting of SEQ ID NO:44 and SEQ ID NO:49,
20 wherein said isolated protein elicits an immune response against a feline Flt-3 ligand protein or has Flt-3 activity;
- (d) (i) an isolated protein of at least about 30 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 90 contiguous nucleotide region identical in sequence to a
25 90 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:55, and SEQ ID NO:57; and
- (ii) an isolated protein of at least about 30 amino acids in length, wherein said protein has an at least 30 contiguous amino acid region identical in sequence to a 30 contiguous amino acid region selected from the group consisting of
30 SEQ ID NO:53, SEQ ID NO:58,

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wherein said isolated protein elicits an immune response against a canine CD40 protein or has CD40 activity;

(e) (i) an isolated protein of at least about 20 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 60 contiguous nucleotide region identical in sequence to a
5 60 contiguous nucleotide region of a nucleic acid sequence comprising SEQ ID NO:60; and

(ii) an isolated protein of at least about 20 amino acids in length, wherein said protein has an at least 20 contiguous amino acid region identical in
10 sequence to a 20 contiguous amino acid region comprising the amino acid sequence SEQ ID NO:61,

wherein said isolated protein elicits an immune response against a feline CD40 protein or has CD40 activity;

(f) (i) an isolated protein of at least about 35 amino acids in
15 length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 105 contiguous nucleotide region identical in sequence to a 105 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:67, and SEQ ID NO:69; and

(ii) an isolated protein of at least about 35 amino acids in
20 length, wherein said protein has an at least 35 contiguous amino acid region identical in sequence to a 35 contiguous amino acid region selected from the group consisting of SEQ ID NO:65 and SEQ ID NO:70,

wherein said isolated protein elicits an immune response against a canine CD154 protein or has CD154 activity;

25 (g) (i) an isolated protein of at least about 50 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 150 contiguous nucleotide region identical in sequence to a 150 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:72, SEQ ID NO:75, and SEQ ID NO:77; and

30 (ii) an isolated protein of at least about 50 amino acids in length, wherein said protein has an at least 50 contiguous amino acid region identical in

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sequence to a 50 contiguous amino acid region selected from the group consisting of SEQ ID NO:73 and SEQ ID NO:78,

wherein said isolated protein elicits an immune response against a feline CD154 protein or has CD154 activity;

5 (h) (i) an isolated protein of at least about 20 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 60 contiguous nucleotide region identical in sequence to a 60 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:80, SEQ ID NO:83, and SEQ ID NO:85; and

10 (ii) an isolated protein of at least about 20 amino acids in length, wherein said protein has an at least 20 contiguous amino acid region identical in sequence to a 20 contiguous amino acid region selected from the group consisting of SEQ ID NO:81 and SEQ ID NO:86,

wherein said isolated protein elicits an immune response against a canine IL-5 protein or has IL-5 activity;

(i) (i) an isolated protein of at least about 15 amino acids in length, wherein said protein is encoded by a nucleic acid molecule, wherein said nucleic acid molecule has an at least 45 contiguous nucleotide region identical in sequence to a 45 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:102, and SEQ ID NO:104; and

(ii) an isolated protein of at least about 15 amino acids in length, wherein said protein has an at least 15 contiguous amino acid region identical in sequence to a 15 contiguous amino acid region selected from the group consisting of SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, and SEQ ID NO:105,

wherein said isolated protein elicits an immune response against a canine IL-13 protein or has IL-13 activity;

(j) (i) an isolated protein encoded by a nucleic acid molecule selected from the group consisting of SEQ ID NO:107, SEQ ID NO:110, SEQ ID NO:113, and SEQ ID NO:116, and

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(ii) an isolated protein selected from the group consisting of SEQ ID NO:108, SEQ ID NO:111, SEQ ID NO:114, and SEQ ID NO:117,

wherein said isolated protein elicits an immune response against a feline interferon alpha protein or has interferon alpha activity;

5 (k) (i) an isolated protein encoded by a nucleic acid molecule selected from the group consisting of SEQ ID NO:119, SEQ ID NO:122, and SEQ ID NO:124, and

(ii) an isolated protein selected from the group consisting of SEQ ID NO:120 and SEQ ID NO:125,

10 wherein said isolated protein elicits an immune response against a feline GM-CSF or has GM-CSF activity;

b. a mimotope of any of said immunoregulatory proteins;

c. a multimeric form of any of said immunoregulatory proteins;

d. an isolated nucleic acid molecule selected from the group consisting of

15 (a) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:19, SEQ ID NO:21 or a homolog thereof, wherein said homolog has an at least 50 contiguous nucleotide region identical in sequence to a 50 contiguous nucleotide region of a nucleic acid sequence selected from the group
20 consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:19, SEQ ID NO:21;

(b) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:25, SEQ ID
25 NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:36, and SEQ ID NO:37, or a homolog thereof, wherein said homolog has an at least 40 contiguous nucleotide region identical in sequence to a 40 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10,
30 SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:28, SEQ

ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:36, and SEQ ID NO:37,;

(c) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, and SEQ ID NO:50, or a homolog thereof, wherein said homolog has an at least 30 contiguous nucleotide region identical in sequence to a 30 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, and SEQ ID NO:50;

(d) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, and SEQ ID NO:59, or a homolog thereof, wherein said homolog has an at least 40 contiguous nucleotide region identical in sequence to a 40 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, and SEQ ID NO:59;

(e) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:60 and SEQ ID NO:62, or a homolog thereof, wherein said homolog has an at least 30 contiguous nucleotide region identical in sequence to a 30 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:60 and SEQ ID NO:62;

(f) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69 and SEQ ID NO:71, or a homolog thereof, wherein said homolog has an at least 45 contiguous nucleotide region identical in sequence to a 45 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69 and SEQ ID NO:71;

(g) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:72, SEQ ID NO:74, SEQ ID

NO:75, SEQ ID NO:76, SEQ ID NO:77, and SEQ ID NO:79, or a homolog thereof, wherein said homolog has an at least 35 contiguous nucleotide region identical in sequence to a 35 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:75, SEQ ID
5 NO:76, SEQ ID NO:77, and SEQ ID NO:79;

(h) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, and SEQ ID NO:87, or a homolog thereof, wherein said homolog has an at least 45 contiguous nucleotide region identical in
10 sequence to a 45 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, and SEQ ID NO:87;

(i) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID
15 NO:90, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, and SEQ ID NO:106, or a homolog thereof, wherein said homolog has an at least 15 contiguous nucleotide region identical in sequence to a 15
contiguous nucleotide region of a nucleic acid sequence selected from the group
20 consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, and SEQ ID NO:106;

(j) an isolated nucleic acid molecule having a nucleic acid sequence
25 selected from the group consisting of SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:116, and SEQ ID NO:118; and

(k) an isolated nucleic acid molecule having a nucleic acid sequence
selected from the group consisting of SEQ ID NO:119, SEQ ID NO:121, SEQ ID
30 NO:122, SEQ ID NO:123, SEQ ID NO:124, and SEQ ID NO:126;

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- e. an antibody that selectively binds to any of said immunoregulatory proteins; and
 - f. an inhibitor of a immunoregulatory protein activity identified by its ability to inhibit the activity of any of said immunoregulatory proteins.
- 5 8. A method to produce an immunoregulatory protein, said method comprising culturing a cell capable of expressing said protein, said protein being encoded by a nucleic acid molecule selected from the group consisting of
- (a) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:4, and SEQ
10 ID NO:19, or a homolog thereof, wherein said homolog has an at least 50 contiguous nucleotide region identical in sequence to a 50 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:4, and SEQ ID NO:19;
 - (b) an isolated nucleic acid molecule comprising a nucleic acid
15 sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:9, SEQ ID NO:22, SEQ ID NO:25, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:33, and SEQ ID NO:36 or a homolog thereof, wherein said homolog has an at least 40 contiguous nucleotide region identical in sequence to a contiguous nucleotide region of a 40
contiguous nucleotide region of a nucleic acid sequence selected from the group
20 consisting of SEQ ID NO:6, SEQ ID NO:9, SEQ ID NO:22, SEQ ID NO:25, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:33, and SEQ ID NO:36;
 - (c) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:46, and SEQ ID NO:48, or a homolog thereof, wherein said
25 homolog has an at least 30 contiguous nucleotide region identical in sequence to a contiguous nucleotide region of a 30 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:46, and SEQ ID NO:48;
 - (d) an isolated nucleic acid molecule comprising a nucleic acid
30 sequence selected from the group consisting of SEQ ID NO:51, SEQ ID NO:52, SEQ ID

- NO:55, and SEQ ID NO:57, or a homolog thereof, wherein said homolog has an at least 40 contiguous nucleotide region identical in sequence to a 40 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:55, and SEQ ID NO:57;
- 5 (e) an isolated nucleic acid molecule comprising a nucleic acid sequence comprising SEQ ID NO:60, or a homolog thereof, wherein said homolog has an at least 30 contiguous nucleotide region identical in sequence to a 30 contiguous nucleotide region of a nucleic acid sequence comprising SEQ ID NO:60;
- (f) an isolated nucleic acid molecule comprising a nucleic acid
10 sequence selected from the group consisting of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:67, and SEQ ID NO:69 or a homolog thereof, wherein said homolog has an at least 45 contiguous nucleotide region identical in sequence to a 45 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:67, and SEQ ID NO:69;
- 15 (g) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:72, SEQ ID NO:75, and SEQ ID NO:77 or a homolog thereof, wherein said homolog has an at least 35 contiguous nucleotide region identical in sequence to a 35 contiguous nucleotide region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:72, SEQ ID
20 NO:75, and SEQ ID NO:77;
- (h) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:80, SEQ ID NO:83, and SEQ ID NO:85, or a homolog thereof, wherein said homolog has an at least 45 contiguous nucleotide region identical in sequence to a 45 contiguous nucleotide region
25 of a nucleic acid sequence selected from the group consisting of SEQ ID NO:80, SEQ ID NO:83, and SEQ ID NO:85;
- (i) an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:99, SEQ ID
30 NO:102, and SEQ ID NO:104, or a homolog thereof, wherein said homolog has an at least 15 contiguous nucleotide region identical in sequence to a 15 contiguous nucleotide

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region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:99, SEQ ID NO:102, and SEQ ID NO:104;

(j) an isolated nucleic acid molecule having a nucleic acid sequence
5 selected from the group consisting of SEQ ID NO:107, SEQ ID NO:110, SEQ ID NO:113, and SEQ ID NO:116; and

(k) an isolated nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO:119, SEQ ID NO:122, and SEQ ID NO:124.

10 9. A method to identify a compound capable of regulating an immune response in an animal, said method comprising:

(a) contacting an isolated canine IL-4 protein with a putative inhibitory compound under conditions in which, in the absence of said compound, said protein has T cell proliferation stimulating activity; and determining if said putative
15 inhibitory compound inhibits said activity;

(b) contacting an isolated canine Flt-3 ligand protein with a putative inhibitory compound under conditions in which, in the absence of said compound, said protein has dendritic precursor cell proliferation stimulating activity; and determining if said putative inhibitory compound inhibits said activity;

20 (c) contacting an isolated feline Flt-3 ligand protein with a putative inhibitory compound under conditions in which, in the absence of said compound, said protein has dendritic precursor cell proliferation stimulating activity; and determining if said putative inhibitory compound inhibits said activity;

(d) contacting an isolated canine CD40 protein with a putative
25 inhibitory compound under conditions in which, in the absence of said compound, said protein has CD40 ligand binding activity; and determining if said putative inhibitory compound inhibits said activity;

(e) contacting an isolated feline CD40 protein with a putative inhibitory compound under conditions in which, in the absence of said compound, said
30 protein has CD40 ligand binding activity; and determining if said putative inhibitory compound inhibits said activity;

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(f) contacting an isolated canine CD154 protein with a putative inhibitory compound under conditions in which, in the absence of said compound, said protein has B cell proliferation activity; and determining if said putative inhibitory compound inhibits said activity;

5 (g) contacting an isolated feline CD154 protein with a putative inhibitory compound under conditions in which, in the absence of said compound, said protein has B cell proliferation activity; and determining if said putative inhibitory compound inhibits said activity;

(h) contacting an isolated canine IL-5 protein with a putative
10 inhibitory compound under conditions in which, in the absence of said compound, said protein has TF-1 cell proliferation activity; and determining if said putative inhibitory compound inhibits said activity;

(i) contacting an isolated canine IL-13 protein with a putative
15 inhibitory compound under conditions in which, in the absence of said compound, said protein has TF-1 cell proliferation activity; and determining if said putative inhibitory compound inhibits said activity;

(j) contacting an isolated feline IFN α protein with a putative
inhibitory compound under conditions in which, in the absence of said compound, said
protein has inhibition of proliferation of GM-CSF stimulated TF-1 cell activity; and
20 determining if said putative inhibitory compound inhibits said activity; or

(k) contacting an isolated feline GMCSF protein with a putative
inhibitory compound under conditions in which, in the absence of said compound, said
protein has TF-1 cell proliferation activity; and determining if said putative inhibitory
compound inhibits said activity.

25 10. The invention as in Claims 1, 2, 3, 6, 7, or 8,
wherein said nucleic acid molecule as set forth in Claim 1(a), 2(a), 3(a), 8(a),
6d.(a), or 7d.(a) comprises a nucleic acid sequence that encodes a canine IL-4 protein;
wherein said nucleic acid molecule as set forth in Claim 1(b), 2(b), 3(b), 8(b),
6d.(b), or 7d.(b) comprises a nucleic acid sequence that encodes a canine Flt-3 ligand
30 protein;

wherein said nucleic acid molecule as set forth in Claim 1(c), 2(c), 3(c), 8(c), 6d.(c), or 7d.(c) comprises a nucleic acid sequence that encodes a feline Flt-3 ligand protein;

wherein said nucleic acid molecule as set forth in Claim 1(d), 2(d), 3(d), 8(d), 6d.(d), or 7d.(d) comprises a nucleic acid sequence that encodes a canine CD40 protein;

wherein said nucleic acid molecule as set forth in Claim 1(e), 2(e), 3(e), 8(e), 6d.(e), or 7d.(e) comprises a nucleic acid sequence that encodes a feline CD40 protein;

wherein said nucleic acid molecule as set forth in Claim 1(f), 2(f), 3(f), 8(f), 6d.(f), or 7d.(f) comprises a nucleic acid sequence that encodes a canine CD154 protein;

wherein said nucleic acid molecule as set forth in Claim 1(g), 2(g), 3(g), 8(g), 6d.(g), or 7d.(g) comprises a nucleic acid sequence that encodes a feline CD154 protein;

wherein said nucleic acid molecule as set forth in Claim 1(h), 2(h), 3(h), 8(h), 6d.(h), or 7d.(h) comprises a nucleic acid sequence that encodes a canine IL-5 protein;

wherein said nucleic acid molecule as set forth in Claim 1(i), 2(i), 3(i), 8(i), 6d.(i), or 7d.(i) comprises a nucleic acid molecule that encodes a canine IL-13 protein;

wherein said nucleic acid molecule as set forth in Claim 1(j), 2(j), 3(j), 8(j), 6d.(j), or 7d.(j) consists of a nucleic acid molecule that encodes a feline interferon alpha protein; and

wherein said nucleic acid molecule as set forth in Claim 1(k), 2(k), 3(k), 8(k), 6d.(k), or 7d.(k) consists of a nucleic acid molecule that encodes a feline GM-CSF.

11. The invention as in Claims 1, 2, 3, 6, 7 or 8,

wherein said nucleic acid molecule of Claim 1(a), 2(a), 3(a), 8(a), 6d.(a), 7d.(a), or 8(a) encodes a protein that elicits an immune response against an IL-4 protein having an amino acid sequence selected from the group consisting of SEQ ID NO:2, and SEQ ID NO:20, or a protein that has IL-4 activity;

wherein said nucleic acid molecule of Claim 1(b), 2(b), 3(b), 6d.(b), 7d.(b), 8(b), 1(c), 2(c), 3(c), 6d.(c), 7d.(c), or 8(c), encodes a protein that elicits an immune response against a Flt-3 ligand protein having an amino acid sequence selected from the group consisting of SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, SEQ ID NO:34, SEQ ID NO:44, and SEQ ID NO:49, or a protein that has Flt-3 ligand activity;

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wherein said nucleic acid molecule of Claim 1(d), 2(d), 3(d), 6d.(d), 7d.(d), 8(d), 1(e), 2(e), 3(e), 6d.(e), 7d.(e), or 8(e) encodes a protein that elicits an immune response against a CD40 protein having an amino acid sequence selected from the group consisting of SEQ ID NO:53, SEQ ID NO:58, and SEQ ID NO:61, or a protein that has
 5 CD40 activity;

wherein said nucleic acid molecule of Claim 1(f), 2(f), 3(f), 6d.(f), 7d.(f), 8(f), 1(g), 2(g), 3(g), 6d.(g), 7d.(g) or 8(g) encodes a protein that elicits an immune response against a CD154 protein having an amino acid sequence selected from the group consisting of SEQ ID NO:65, SEQ ID NO:70, SEQ ID NO:73, and SEQ ID NO:78, or a
 10 protein that has CD154 activity;

wherein said nucleic acid molecule of Claim 1(h), 2(h), 3(h), 8(h), 6d.(h), or 7d.(h) encodes a protein that elicits an immune response against an IL-5 protein having an amino acid sequence selected from the group consisting of SEQ ID NO:81 and SEQ ID NO:86, or a protein that has IL-5 activity;

15 wherein said nucleic acid molecule of Claim 1(i), 2(i), 3(i), 6d.(i), 7d.(i), or 8(i) encodes a protein that elicits an immune response against an IL-13 protein having an amino acid sequence selected from the group consisting of SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, and SEQ ID NO:105, or a protein that has IL-13 activity;

wherein said nucleic acid molecule of Claim 1(j), 2(j), 3(j), 6d.(j), 7d.(j), or 8(j)
 20 encodes a protein that elicits an immune response against an interferon alpha protein having an amino acid sequence selected from the group consisting of SEQ ID NO:108, SEQ ID NO:111, SEQ ID NO:114 and SEQ ID NO:117; and

wherein said nucleic acid molecule of Claim 1(k), 2(k), 3(k), 6d.(k), 7d.(k), or 8(k) encodes a protein that elicits an immune response against a GM-CSF protein having
 25 an amino acid sequence selected from the group consisting of SEQ ID NO:120 and SEQ ID NO:125.

12. The invention as in Claims 1, 2, 3, 6, 7, or 8, wherein said nucleic acid molecule comprises a nucleic acid molecule selected from the group consisting of
 nCaIL-4₅₄₉, nCaIL-4₃₉₆, nCaIL-4₃₂₄, nCaFlt3L₁₀₁₃, nCaFlt3L₈₈₂, nCaFlt3L₈₀₄, nCaFlt3L₈₂₈,
 30 nCaFlt3L₉₈₅, nCaFlt3L₁₀₁₉, nCaFlt3L₉₃, nCaFlt3L₇₅₀, nFeFlt3L₃₉₅, nFeFlt3L₇₉₃,
 nFeFlt3L₉₄₂, nFeFlt3L₈₇₃, nFeFlt3L₇₉₅, nCaCD40₃₂₁, nCaCD40₁₄₂₅, nCaCD40₈₂₂,

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nCaCD40₇₆₅, nFeCD40₃₃₆, nCaCD154₃₉₀, nCaCD154₈₇₈, nCaCD154₇₈₀, nCaCD154₆₃₃,
 nFeCD154₈₈₅, nFeCD154₇₈₀, nFeCD154₆₃₃, nCaIL-5₆₁₀, nCaIL-5₄₀₂, nCaIL-5₃₄₅, nCaIL-
 13₁₆₆, nCaIL-13₂₇₂, nCaIL-13₂₇₈, nCaIL-13₁₃₀₂, nCaIL-13₃₉₃, nCaIL-13₃₃₃, nCaIL-13₁₂₆₉,
 nCaIL-13₃₉₀, nCaIL-13₃₃₀, nFeIFN α _{567a}, nFeIFN α _{567b}, nFeIFN α _{498a}, nFeIFN α _{498b},
 5 nFeGMCSF₄₄₄, nFeGMCSF₄₃₂, and nFeGMCSF₃₈₁.

13. The invention as in Claims 1, 2, 3, 6, 7, or 8, wherein said nucleic acid molecule is selected from the group consisting of:

(a) a nucleic acid molecule comprising a nucleic acid sequence that encodes a protein having an amino acid sequence selected from the group consisting of

10 (i) SEQ ID NO:2, SEQ ID NO:20, SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, SEQ ID NO:34, SEQ ID NO:44, SEQ ID NO:49, SEQ ID NO:53, SEQ ID NO:58, SEQ ID NO:61, SEQ ID NO:65, SEQ ID NO:70, SEQ ID NO:73, SEQ ID NO:78, SEQ ID NO:81, SEQ ID NO:86, SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, SEQ ID NO:105, and

15 (ii) SEQ ID NO:108, SEQ ID NO:111, SEQ ID NO:114, SEQ ID NO:117, SEQ ID NO:120, and SEQ ID NO:125; and

(b) a nucleic acid molecule comprising an allelic variant of a nucleic acid molecule encoding a protein having any of said amino acid sequences of group (a) (i).

20 14. The invention as in Claims 1, 2, 3, 6, 7, or 8, wherein said nucleic acid molecule is selected from the group consisting of:

(a) a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of

25 (i) SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID
 30 NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:62, SEQ ID

NO:63, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:106, and

(ii) SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124; and SEQ ID NO:126; and

(b) a nucleic acid molecule comprising an allelic variant of a nucleic acid molecule comprising any of said nucleic acid sequences of (a) (i).

15. The invention as in Claims 1, 2, 3, 6, 7, or 8, wherein said nucleic acid molecule is an oligonucleotide.

16. A recombinant molecule comprising a nucleic acid molecule as set forth in Claims 1, 2, 3, 6, 7, or 8, operatively linked to a transcription control sequence.

17. A recombinant virus comprising a nucleic acid molecule as set forth in Claims 1, 2, 3, 6, 7, or 8.

20. 18. A recombinant cell comprising a nucleic acid molecule as set forth in Claims 1, 2, 3, 6, 7, or 8.

19. The invention as in Claims 4, 5, 6, 7 or 8, wherein said protein of Claim 4(a), 5(a), 6a.(a), 6b., 6c., 7a.(a), 7b., 7c., or 8(a) is selected from the group consisting of: (i) an amino acid sequence selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:20; and (ii) a protein encoded by an allelic variant of a nucleic acid molecule encoding a protein selected from the group consisting of SEQ ID NO:2 and SEQ ID NO:20;

wherein said protein of Claim 4(b), 5(b), 6a.(b), 6b., 6c., 7a.(b), 7b., 7c., or 8(b) is selected from the group consisting of: (i) an amino acid sequence selected from the group consisting of SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, and SEQ ID NO:34; and (ii) a protein encoded by an allelic variant of a nucleic acid

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molecule encoding a protein selected from the group consisting of SEQ ID NO:7, SEQ ID NO:23, SEQ ID NO:26, SEQ ID NO:31, and SEQ ID NO:34;

wherein said protein of Claim 4(c), 5(c), 6a.(c), 6b., 6c., 7a.(c), 7b., 7c., or 8(c) is selected from the group consisting of: (i) an amino acid sequence selected from the group consisting of SEQ ID NO:44 and SEQ ID NO:49; and (ii) a protein encoded by an allelic variant of a nucleic acid molecule encoding a protein selected from the group consisting of SEQ ID NO:44 and SEQ ID NO:49;

wherein said protein of Claim 4(d), 5(d), 6a.(d), 6b., 6c., 7a.(d), 7b., 7c., or 8(d) is selected from the group consisting of: (i) an amino acid sequence selected from the group consisting of SEQ ID NO:53 and SEQ ID NO:58; and (ii) a protein encoded by an allelic variant of a nucleic acid molecule encoding a protein selected from the group consisting of SEQ ID NO:53 and SEQ ID NO:58;

wherein said protein of Claim 4(e), 5(e), 6a.(e), 6b., 6c., 7a.(e), 7b., 7c., or 8(e) is selected from the group consisting of: (i) an amino acid sequence comprising SEQ ID NO:61; and a protein encoded by an allelic variant of a nucleic acid molecule encoding the protein SEQ ID NO:61;

wherein said protein of Claim 4(f), 5(f), 6a.(f), 6b., 6c., 7a.(f), 7b., 7c., or 8(f) is selected from the group consisting of: (i) an amino acid sequence selected from the group consisting of SEQ ID NO:65 and SEQ ID NO:70; and (ii) a protein encoded by an allelic variant of a nucleic acid molecule encoding a protein selected from the group consisting of SEQ ID NO:65 and SEQ ID NO:70;

wherein said protein of Claim 4(g), 5(g), 6a.(g), 6b., 6c., 7a.(g), 7b., 7c., or 8(g) is selected from the group consisting of: (i) an amino acid sequence selected from the group consisting of SEQ ID NO:73 and SEQ ID NO:78; and (ii) a protein encoded by an allelic variant of a nucleic acid molecule encoding a protein selected from the group consisting of SEQ ID NO:73 and SEQ ID NO:78;

wherein said protein of Claim 4(h), 5(h), 6a.(h), 6b., 6c., 7a.(h), 7b., 7c., or 8(h) is selected from the group consisting of: (i) an amino acid sequence selected from the group consisting of SEQ ID NO:81 and SEQ ID NO:86; and (ii) a protein encoded by an allelic variant of a nucleic acid molecule encoding a protein selected from the group consisting of SEQ ID NO:81 and SEQ ID NO:86;

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wherein said protein of Claim 4(i), 5(i), 6a.(i), 6b., 6c., 7a.(i), 7b., 7c., or 8(i). is selected from the group consisting of: (i) SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, and SEQ ID NO:105; and (ii) a protein encoded by an allelic variant of a nucleic acid molecule encoding a protein selected from the group consisting of SEQ ID NO:92, SEQ ID NO:97, SEQ ID NO:100, and SEQ ID NO:105;

wherein said protein of Claim 4(j), 5(j), 6a.(j), 6b., 6c., 7a.(j), 7b., 7c., or 8(j) is selected from the group consisting of SEQ ID NO:108, SEQ ID NO:111, SEQ ID NO:114, and SEQ ID NO:117; and

wherein said protein of Claim 4(k), 5(k), 6a.(k), 6b., 6c., 7a.(k), 7b., 7c., or 8(k) is selected from the group consisting of SEQ ID NO:120 and SEQ ID NO:125.

20. An isolated antibody that selectively binds to a protein as set forth in Claims 4, 5, 6, or 7.

21. The invention as in Claim 6 or 7, wherein said composition further comprises a component selected from the group consisting of an excipient, an adjuvant and a carrier.

22. The invention as in Claim 6 or 7, wherein said compound is selected from the group consisting of a naked nucleic acid vaccine and a recombinant cell vaccine.

23. The method of Claim 7 or 9, wherein said animal is selected from the group consisting of canids and felids.

SEQUENCE LISTING

<110> Sim, Gek-Kee
 Yang, Shumin
 Dreitz, Matthew J.
 Wonderling, Ramani S.

<120> CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
 ACID MOLECULES, AND USES THEREOF

<130> IM-2-C1-PCT

<140> not yet assigned

<141> 1999-05-28

<150> 60/087,306

<151> 1998-05-29

<160> 154

<170> PatentIn Ver. 2.0

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 Ser Gln Leu Ile Pro Thr Leu Val Cys Leu Leu Ala Leu Thr Ser Thr
 5 10 15 20

ttt gtc cac gga cat aac ttc aat att act att aaa gag atc atc aaa 150
 Phe Val His Gly His Asn Phe Asn Ile Thr Ile Lys Glu Ile Ile Lys
 25 30 35

atg ttg aac atc ctc aca gcg aga aac gac tcg tgc atg gag ctg act 198
 Met Leu Asn Ile Leu Thr Ala Arg Asn Asp Ser Cys Met Glu Leu Thr
 40 45 50

gtc aag gac gtc ttc act gct cca aag aac aca agc gat aag gaa atc 246
 Val Lys Asp Val Phe Thr Ala Pro Lys Asn Thr Ser Asp Lys Glu Ile
 55 60 65

ttc tgc aga gct gct act gta ctg cgg cag atc tat aca cac aac tgc 294
 Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Ile Tyr Thr His Asn Cys
 70 75 80

tcc aac aga tat ctc aga gga ctc tac agg aac ctc agc agc atg gca 342
 Ser Asn Arg Tyr Leu Arg Gly Leu Tyr Arg Asn Leu Ser Ser Met Ala
 85 90 95 100

aac aag acc tgt tct atg aat gaa atc aag aag agt aca ctg aaa gac 390
 Asn Lys Thr Cys Ser Met Asn Glu Ile Lys Lys Ser Thr Leu Lys Asp
 105 110 115

ttc ttg gaa agg cta aaa gtg atc atg cag aag aaa tac tac agg cat 438
 Phe Leu Glu Arg Leu Lys Val Ile Met Gln Lys Lys Tyr Tyr Arg His
 120 125 130

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atttataaca taataaaata aaatatatat agaaaaaaaa aaaaaaaaaa a 549

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Glu Ile Ile Lys Met Leu Asn Ile Leu Thr Ala Arg Asn Asp Ser Cys
 35 40 45

Met Glu Leu Thr Val Lys Asp Val Phe Thr Ala Pro Lys Asn Thr Ser
 50 55 60

Asp Lys Glu Ile Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Ile Tyr
 65 70 75 80

Thr His Asn Cys Ser Asn Arg Tyr Leu Arg Gly Leu Tyr Arg Asn Leu
 85 90 95

Ser Ser Met Ala Asn Lys Thr Cys Ser Met Asn Glu Ile Lys Lys Ser
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Tyr Tyr Arg His
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 gtatttcttc tgcattgatca ctttttagcct ttccaagaag tctttcagtg tacttcttctt 180
 gatttcattc atagaacagg tcttggttgc catgctgctg aggttcctgt agagtcctct 240
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 gaagatttcc ttatcgcttg tgttctttgg agcagtgaag acgtccttga cagtcagctc 360
 catgcacgag tcgtttctcg ctgtgaggat gttcaacatt ttgatgatct ctttaatagt 420
 aatattgaag ttatgtccgt ggacaaaggt gctgggtgagt gctagtaagc agaccagagt 480
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ctcacagcga gaaacgactc gtgcatggag ctgactgtca aggacgtctt cactgctcca 180
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 acacacaact gctccaacag atatctcaga ggactctaca ggaacctcag cagcatggca 300
 aacaagacct gttctatgaa tgaaatcaag aagagtacac tgaaagactt cttggaaagg 360
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 tttaatagta atattgaagt tatgtccgtg gacaaagggtg ctgggtgagtg ctagtaagca 360
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 1 5

tgg agc cca act gcc tcc ctg ttg ctg ctg ctg ctg ctc agc ccc ggc 103
 Trp Ser Pro Thr Ala Ser Leu Leu Leu Leu Leu Leu Ser Pro Gly

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ctc cgc ggg acc ccc gac tgc tcc ttc agc cac agc ccc atc tcc tcc			151
Leu Arg Gly Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser			
25	30	35	
acc ttc gcg gtc acc atc cgc aag ctg tct gat tac ctg ctt cag gac			199
Thr Phe Ala Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp			
40	45	50	55
tat cca gtc act gtc gcc tcc aac ctg cag gac gac gag ctc tgc ggg			247
Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly			
	60	65	70
gcg ttc tgg cgc ctg gtc ctg gcc cag cgc tgg atg gtg cgg ctc cag			295
Ala Phe Trp Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln			
	75	80	85
gct gtg gct gga tcc caa atg caa atc ctg ctg gag gct gtc aac acg			343
Ala Val Ala Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr			
	90	95	100
gag ata cac ttt gtc acc ttc tgt gcc ttc cag ccc ctc ccc agc tgt			391
Glu Ile His Phe Val Thr Phe Cys Ala Phe Gln Pro Leu Pro Ser Cys			
	105	110	115
ctt cgc ttc gtc cag acc aac atc tcc cac ctc ctg cag gac acc tcc			439
Leu Arg Phe Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser			
120	125	130	135
cag cag ctg gcc gcc ctg aag ccc tgg atc acc cgc agg aat ttc tcc			487
Gln Gln Leu Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser			
	140	145	150
ggg tgc ctg gag ctg cag tgt cag ccc gac tcc tct aca ttg gtg ccc			535
Gly Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro			
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cca agg agc ccc ggg gcc ctg gag gcc act gcc ttg cca gcc cct cag			583
Pro Arg Ser Pro Gly Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln			
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gca cct cgg ctg ctc ctc ctg ctg ctg ctg ccc gtg gct ctc ctg ctg			631
Ala Pro Arg Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu			
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Met Ser Thr Ala Trp Cys Leu His Trp Arg Arg Arg Arg Arg Arg Arg			

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 Ser Pro Tyr Pro Gly Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser
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 Thr Gly Pro Phe Leu Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly
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 Pro Leu Pro Leu Cys Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile
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 Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
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 Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp Arg Leu Val Leu Ala Gln
 65 70 75 80

Arg Trp Met Val Arg Leu Gln Ala Val Ala Gly Ser Gln Met Gln Ile
 85 90 95

 Leu Leu Glu Ala Val Asn Thr Glu Ile His Phe Val Thr Phe Cys Ala
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 Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 115 120 125

 His Leu Leu Gln Asp Thr Ser Gln Gln Leu Ala Ala Leu Lys Pro Trp
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 Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu Gln Cys Gln Pro
 145 150 155 160

 Asp Ser Ser Thr Leu Val Pro Pro Arg Ser Pro Gly Ala Leu Glu Ala
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 Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu Leu Leu Leu Leu
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<210> 14

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<212> DNA

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1				5				10					15			

ctc	aca	gcg	aga	aac	gac	tcg	tgc	atg	gag	ctg	act	gtc	aag	gac	gtc	96
Leu	Thr	Ala	Arg	Asn	Asp	Ser	Cys	Met	Glu	Leu	Thr	Val	Lys	Asp	Val	
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ttc	act	gct	cca	aag	aac	aca	agc	gat	aag	gaa	atc	ttc	tgc	aga	gct	144
Phe	Thr	Ala	Pro	Lys	Asn	Thr	Ser	Asp	Lys	Glu	Ile	Phe	Cys	Arg	Ala	
		35						40					45			

gct	act	gta	ctg	cgg	cag	atc	tat	aca	cac	aac	tgc	tcc	aac	aga	tat	192
Ala	Thr	Val	Leu	Arg	Gln	Ile	Tyr	Thr	His	Asn	Cys	Ser	Asn	Arg	Tyr	
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ctc aga gga ctc tac agg aac ctc agc agc atg gca aac aag acc tgt 240
 Leu Arg Gly Leu Tyr Arg Asn Leu Ser Ser Met Ala Asn Lys Thr Cys
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tct atg aat gaa atc aag aag agt aca ctg aaa gac ttc ttg gaa agg 288
 Ser Met Asn Glu Ile Lys Lys Ser Thr Leu Lys Asp Phe Leu Glu Arg
 85 90 95

cta aaa gtg atc atg cag aag aaa tac tac agg cat 324
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Phe Thr Ala Pro Lys Asn Thr Ser Asp Lys Glu Ile Phe Cys Arg Ala
 35 40 45

Ala Thr Val Leu Arg Gln Ile Tyr Thr His Asn Cys Ser Asn Arg Tyr
 50 55 60

Leu Arg Gly Leu Tyr Arg Asn Leu Ser Ser Met Ala Asn Lys Thr Cys
 65 70 75 80

Ser Met Asn Glu Ile Lys Lys Ser Thr Leu Lys Asp Phe Leu Glu Arg
 85 90 95

Leu Lys Val Ile Met Gln Lys Lys Tyr Tyr Arg His
 100 105

<210> 21

<211> 324

<212> DNA

<213> Canis familiaris

<400> 21

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actcttcttg atttcattca tagaacaggt cttgtttgcc atgctgctga ggttcctgta 120
 gagtcctctg agatatctgt tggagcagtt gtgtgtatag atctgccgca gtacagtagc 180
 agctctgcag aagatttcct tatcgcttgt gttctttgga gcagtgaaga cgtccttgac 240
 agtcagctcc atgcacgagt cgtttctcgc tgtgaggatg ttcaacattt tgatgatctc 300
 tttaatagta atattgaagt tatg 324

<210> 22

<211> 804

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(804)

<400> 22

acc ccc gac tgc tcc ttc agc cac agc ccc atc tcc tcc acc ttc gcg 48
 Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Ala
 1 5 10 15

gtc acc atc cgc aag ctg tct gat tac ctg ctt cag gac tat cca gtc 96
 Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val
 20 25 30

act gtc gcc tcc aac ctg cag gac gac gag ctc tgc ggg gcg ttc tgg 144
 Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp
 35 40 45

cgc ctg gtc ctg gcc cag cgc tgg atg gtg cgg ctc cag gct gtg gct 192
 Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala
 50 55 60

gga tcc caa atg caa atc ctg ctg gag gct gtc aac acg gag ata cac 240
 Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His
 65 70 75 80

ttt gtc acc ttc tgt gcc ttc cag ccc ctc ccc agc tgt ctt cgc ttc 288
 Phe Val Thr Phe Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe
 85 90 95

gtc cag acc aac atc tcc cac ctc ctg cag gac acc tcc cag cag ctg 336
 Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Gln Gln Leu

100	105	110	
gcc gcc ctg aag ccc tgg atc acc cgc agg aat ttc tcc ggg tgc ctg			384
Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu			
115	120	125	
gag ctg cag tgt cag ccc gac tcc tct aca ttg gtg ccc cca agg agc			432
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser			
130	135	140	
ccc ggg gcc ctg gag gcc act gcc ttg cca gcc cct cag gca cct cgg			480
Pro Gly Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg			
145	150	155	160
ctg ctc ctc ctg ctg ctg ctg ccc gtg gct ctc ctg ctg atg tcc act			528
Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Thr			
165	170	175	
gcc tgg tgc ctg cat tgg cga agg agg cgg cgg cgg agg tca ccc tac			576
Ala Trp Cys Leu His Trp Arg Arg Arg Arg Arg Arg Arg Ser Pro Tyr			
180	185	190	
cct ggg gag cag agg aca ctg agg ccc agc gag cgg agc cat ctg ccc			624
Pro Gly Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro			
195	200	205	
gag gac aca gag ctg gga cct gga ggg agt cag cta gag act ggt ccc			672
Glu Asp Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro			
210	215	220	
ttc ctc gac cac gca gcc ccg ctc gct ccc tcc cca gga tca agg caa			720
Phe Leu Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln			
225	230	235	240
cgc ccg ccc cca acg ccc cca aag cca gcc cca gcc cca cct ctc ccc			768
Arg Pro Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro			
245	250	255	
ctc tgt aca aag tcc ttg ccc cca aga aat tgt ata			804
Leu Cys Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile			
260	265		

<210> 23

<211> 268

<212> PRT

<213> Canis familiaris

<400> 23

Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Ala
 1 5 10 15

Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val
 20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp
 35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala
 50 55 60

Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His
 65 70 75 80

Phe Val Thr Phe Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe
 85 90 95

Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Gln Gln Leu
 100 105 110

Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu
 115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser
 130 135 140

Pro Gly Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg
 145 150 155 160

Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Thr
 165 170 175

Ala Trp Cys Leu His Trp Arg Arg Arg Arg Arg Arg Arg Ser Pro Tyr
 180 185 190

Pro Gly Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro
 195 200 205

Glu Asp Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro
 210 215 220

Phe Leu Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln
 225 230 235 240

Arg Pro Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro
 245 250 255

Leu Cys Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile
 260 265

<210> 24

<211> 804

<212> DNA

<213> Canis familiaris

<400> 24

tatacaattt cttgggggca aggactttgt acagaggggg agaggtgggg ctggggctgg 60
 ctttgggggc gttgggggcg ggcgttgect tgatcctggg gagggagcga gcggggctgc 120
 gtggtcgagg aagggaccag tctctagctg actcctcca ggtcccagct ctgtgtcctc 180
 gggcagatgg ctccgctcgc tgggcctcag tgtcctctgc tcccagggt agggtgacct 240
 ccgccgccgc ctcttcgcc aatgcaggca ccaggcagtg gacatcagca ggagagccac 300
 gggcagcagc agcaggagga gcagccgagg tgcttgagg gctggcaagg cagtggcctc 360
 cagggccccc gggctccttg ggggcaccaa tgtagaggag tcgggctgac actgcagctc 420
 caggcacccc gagaaattcc tgccgggtgat ccagggcttc agggcggcca gctgctggga 480
 ggtgtcctgc aggaggtggg agatgttggt ctggacgaag cgaagacagc tggggagggg 540
 ctggaaggca cagaaggtga caaagtgtat ctccgtgttg acagcctcca gcaggatttg 600
 catttgggat ccagccacag cctggagccg caccatccag cgctgggcca ggaccaggcg 660
 ccagaacgcc ccgcagagct cgctgtcctg caggttggag gcgacagtga ctggatagtc 720
 ctgaagcagg taatcagaca gcttgccgat ggtgaccgag aaggtggagg agatggggct 780
 gtggctgaag gagcagtcgg gggt 804

<210> 25

<211> 985

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (74)..(901)

<400> 25

ccggcctggc cccttccacg cccagctggg gcaagcctga tctgaccata ggcatgaggg 60

gcctccggcc gag atg ata gtg ctg gcg cca gcc tgg agc cca act gcc 109

Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Ala

1

5

10

tcc ctg ttg ctg ctg ctg ctg ctc agc ccc ggc ctc cgc ggg acc ccc 157

Ser Leu Leu Leu Leu Leu Leu Leu Ser Pro Gly Leu Arg Gly Thr Pro

15

20

25

gac tgc tcc ttc agc cac agc ccc atc tcc tcc acc ttc gcg gtc acc 205

Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Ala Val Thr

30

35

40

atc cgc aag ctg tct gat tac ctg ctt cag gac tat cca gtc act gtc 253

Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val

45

50

55

60

gcc tcc aac ctg cag gac gac gag ctc tgc ggg gcg ttc tgg cgc ctg 301

Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp Arg Leu

65

70

75

gtc ctg gcc cag cgc tgg atg gtg cgg ctc cag gct gtg gct gga tcc 349

Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala Gly Ser

80

85

90

caa atg caa atc ctg ctg gag gct gtc aac acg gag ata cac ttt gtc 397

Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His Phe Val

95

100

105

acc ttc tgt gcc ttc cag gac acc tcc cag cag ctg gcc gcc ctg aag 445

Thr Phe Cys Ala Phe Gln Asp Thr Ser Gln Gln Leu Ala Ala Leu Lys

110

115

120

ccc tgg atc acc cgc agg aat ttc tcc ggg tgc ctg gag ctg cag tgt 493

Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu Gln Cys

125

130

135

140

cag ccc gac tcc tct aca ttg gtg ccc cca agg agc ccc ggg gcc ctg 541

Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser Pro Gly Ala Leu

145

150

155

gag gcc act gcc ttg cca gcc cct cag gca cct cgg ctg ctc ctc ctg 589

Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu Leu Leu

160

165

170

ctg ctg ctg ccc gtg gct ctc ctg ctg atg tcc act gcc tgg tgc ctg 637
 Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Thr Ala Trp Cys Leu
 175 180 185

cat tgg cga agg agg cgg cgg cgg agg tca ccc tac cct ggg gag cag 685
 His Trp Arg Arg Arg Arg Arg Arg Arg Ser Pro Tyr Pro Gly Glu Gln
 190 195 200

agg aca ctg agg ccc agc gag cgg agc cat ctg ccc gag gac aca gag 733
 Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro Glu Asp Thr Glu
 205 210 215 220

ctg gga cct gga ggg agt cag cta gag act ggt ccc ttc ctc gac cac 781
 Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu Asp His
 225 230 235

gca gcc ccg ctc gct ccc tcc cca gga tca agg caa cgc ccg ccc cca 829
 Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro Pro Pro
 240 245 250

acg ccc cca aag cca gcc cca gcc cca cct ctc ccc ctc tgt aca aag 877
 Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro Leu Cys Thr Lys
 255 260 265

tcc ttg ccc cca aga aat tgt ata taaatcatcc ttttctacca gcaaaaaaaaa 931
 Ser Leu Pro Pro Arg Asn Cys Ile
 270 275

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 985

<210> 26

<211> 276

<212> PRT

<213> Canis familiaris

<400> 26

Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Ala Ser Leu Leu Leu
 1 5 10 15

Leu Leu Leu Leu Ser Pro Gly Leu Arg Gly Thr Pro Asp Cys Ser Phe
 20 25 30

Ser His Ser Pro Ile Ser Ser Thr Phe Ala Val Thr Ile Arg Lys Leu
 35 40 45

Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
 50 55 60

Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp Arg Leu Val Leu Ala Gln
 65 70 75 80
 Arg Trp Met Val Arg Leu Gln Ala Val Ala Gly Ser Gln Met Gln Ile
 85 90 95
 Leu Leu Glu Ala Val Asn Thr Glu Ile His Phe Val Thr Phe Cys Ala
 100 105 110
 Phe Gln Asp Thr Ser Gln Gln Leu Ala Ala Leu Lys Pro Trp Ile Thr
 115 120 125
 Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser
 130 135 140
 Ser Thr Leu Val Pro Pro Arg Ser Pro Gly Ala Leu Glu Ala Thr Ala
 145 150 155 160
 Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu Leu Leu Leu Leu Pro
 165 170 175
 Val Ala Leu Leu Leu Met Ser Thr Ala Trp Cys Leu His Trp Arg Arg
 180 185 190
 Arg Arg Arg Arg Arg Ser Pro Tyr Pro Gly Glu Gln Arg Thr Leu Arg
 195 200 205
 Pro Ser Glu Arg Ser His Leu Pro Glu Asp Thr Glu Leu Gly Pro Gly
 210 215 220
 Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu Asp His Ala Ala Pro Leu
 225 230 235 240
 Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro Pro Pro Thr Pro Pro Lys
 245 250 255
 Pro Ala Pro Ala Pro Pro Leu Pro Leu Cys Thr Lys Ser Leu Pro Pro
 260 265 270
 Arg Asn Cys Ile
 275

<210> 27

<211> 985

<212> DNA

<213> Canis familiaris

<400> 27

tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60
ttgctggtag aaaaggatga tttatatata atttcttggg ggcaaggact ttgtacagag 120
ggggagaggt ggggctgggg ctggcttttg gggcgttggg ggcgggctt gccttgatcc 180
tggggagggg gcgagcgggg ctgcgtgggc gaggaaggga ccagtctcta gctgactccc 240
tccaggcccc agctctgtgt cctcgggcag atggctccgc tcgctgggccc tcagtgtcct 300
ctgctcccca gggtagggtg acctccgccg ccgcctcctt cgccaatgca ggcaccaggc 360
agtggacatc agcaggagag ccacgggcag cagcagcagg aggagcagcc gaggtgcctg 420
aggggctggc aaggcagtgg cctccagggc cccggggctc cttgggggca ccaatgtaga 480
ggagtcgggc tgacactgca gctccaggca cccggagaaa ttcttgccgg tgatccaggg 540
cttcagggcg gccagctgct gggaggtgtc ctggaaggca cagaaggta caaagtgtat 600
ctccgtgttg acagcctcca gcaggatttg catttgggat ccagccacag cctggagccg 660
caccatccag cgctggggca ggaccaggcg ccagaacgcc ccgcagagct cgtcgtcctg 720
caggttggag gcgacagtga ctggatagtc ctgaagcagg taatcagaca gcttgccgat 780
ggtgaccgcg aagggtggagg agatggggct gtggctgaag gagcagtcgg gggccccgcg 840
gaggccgggg ctgagcagca gcagcagcaa cagggaggca gttgggctcc aggctggcgc 900
cagcactatc atctcggccg gaggcccctc atgcctatgg tcagatcagg cttgccccag 960
ctgggcgtgg aaggggccag gccgg 985

<210> 28

<211> 828

<212> DNA

<213> Canis familiaris

<400> 28

atgatagtgc tggegcagc ctggagccca actgcctccc tggtgctgct gctgctgctc 60
agccccggcc tccgcgggac ccccgactgc tccttcagcc acagccccat ctctccacc 120
ttcgcgggtca ccatccgcaa gctgtctgat tacctgcttc aggactatcc agtcactgtc 180

gcctccaacc tgcaggacga cgagctctgc ggggcgttct ggcgcctggc cctggcccag 240
cgctggatgg tgcggctcca ggctgtggct ggatcccaaa tgcaaatact gctggaggct 300
gtcaacacgg agatacactt tgtaaccttc tgtgccttcc aggacacctc ccagcagctg 360
gccgccctga agccctggat caccgcagg aatttctccg ggtgcctgga gctgcagtgt 420
cagcccgact cctctacatt ggtgccccca aggagccccg gggccctgga ggccactgcc 480
ttgccagccc ctccaggacc tcggctgctc ctctgtctgc tgctgcccggt ggctctcctg 540
ctgatgtcca ctgcctgggtg cctgcattgg cgaaggaggc ggcggcggag gtcaccctac 600
cctggggagc agaggacact gaggcccagc gagcggagcc atctgcccga ggacacagag 660
ctgggacctg gagggagtca gctagagact ggtcccttcc tcgaccacgc agccccgctc 720
gtccctccc caggatcaag gcaacgccg cccccaacgc ccccaaagcc agccccagcc 780
ccacctctcc ccctctgtac aaagtccttg cccccaagaa attgtata 828

<210> 29

<211> 828

<212> DNA

<213> *Canis familiaris*

<400> 29

tatacaattt cttgggggca aggactttgt acagaggggg agaggtgggg ctggggctgg 60
ctttgggggc gttggggggc ggcgttgctt tgatcctggg gagggagcga gcggggctgc 120
gtggctcagg aagggaccag tctctagctg actccctcca ggtcccagct ctgtgtcctc 180
gggcagatgg ctccgctcgc tgggcctcag tgctctctgc tcccagggt agggtgacct 240
ccgccgccgc ctcttctgcc aatgcaggca ccaggcagtg gacatcagca ggagagccac 300
gggcagcagc agcaggagga gcagccgagg tgcttgaggg gctggcaagg cagtggcctc 360
cagggccccg gggctccttg ggggcaccaa tgtagaggag tcgggctgac actgcagctc 420
caggcaccgc gagaaattcc tgcgggtgat ccagggttc agggcgcca gctgctggga 480
ggtgtcctgg aaggcacaga aggtgacaaa gtgtatctcc gtgttgacag cctccagcag 540

gatttgcat tgggatccag ccacagcctg gagccgcacc atccagcgct gggccaggac 600
 caggcgccag aacgccccgc agagctcgtc gtcctgcagg ttggaggcga cagtgactgg 660
 atagtcctga agcaggtaat cagacagctt gcggatgggtg accgcgaagg tggaggagat 720
 ggggctgtgg ctgaaggagc agtcgggggt cccgcggagg ccggggctga gcagcagcag 780
 cagcaacagg gaggcagttg ggctccaggc tggcgccagc actatcat 828

<210> 30

<211> 750

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(750)

<400> 30

acc ccc gac tgc tcc ttc agc cac agc ccc atc tcc tcc acc ttc gcg 48
 Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Ala
 1 5 10 15

gtc acc atc cgc aag ctg tct gat tac ctg ctt cag gac tat cca gtc 96
 Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val
 20 25 30

act gtc gcc tcc aac ctg cag gac gac gag ctc tgc ggg gcg ttc tgg 144
 Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp
 35 40 45

cgc ctg gtc ctg gcc cag cgc tgg atg gtg cgg ctc cag gct gtg gct 192
 Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala
 50 55 60

gga tcc caa atg caa atc ctg ctg gag gct gtc aac acg gag ata cac 240
 Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His
 65 70 75 80

ttt gtc acc ttc tgt gcc ttc cag gac acc tcc cag cag ctg gcc gcc 288
 Phe Val Thr Phe Cys Ala Phe Gln Asp Thr Ser Gln Gln Leu Ala Ala
 85 90 95

ctg aag ccc tgg atc acc cgc agg aat ttc tcc ggg tgc ctg gag ctg 336
 Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu
 100 105 110

cag tgt cag ccc gac tcc tct aca ttg gtg ccc cca agg agc ccc ggg 384
 Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser Pro Gly
 115 120 125

gcc ctg gag gcc act gcc ttg cca gcc cct cag gca cct cgg ctg ctc 432
 Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu
 130 135 140

ctc ctg ctg ctg ctg ccc gtg gct ctc ctg ctg atg tcc act gcc tgg 480
 Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Thr Ala Trp
 145 150 155 160

tgc ctg cat tgg cga agg agg cgg cgg cgg agg tca ccc tac cct ggg 528
 Cys Leu His Trp Arg Arg Arg Arg Arg Arg Arg Ser Pro Tyr Pro Gly
 165 170 175

gag cag agg aca ctg agg ccc agc gag cgg agc cat ctg ccc gag gac 576
 Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro Glu Asp
 180 185 190

aca gag ctg gga cct gga ggg agt cag cta gag act ggt ccc ttc ctc 624
 Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu
 195 200 205

gac cac gca gcc ccg ctc gct ccc tcc cca gga tca agg caa cgc ccg 672
 Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro
 210 215 220

ccc cca acg ccc cca aag cca gcc cca gcc cca cct ctc ccc ctc tgt 720
 Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro Leu Cys
 225 230 235 240

aca aag tcc ttg ccc cca aga aat tgt ata 750
 Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile
 245 250

<210> 31

<211> 250

<212> PRT

<213> Canis familiaris

<400> 31

Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Ala
 1 5 10 15

Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val

	20	25	30
Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp	35	40	45
Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala	50	55	60
Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His	65	70	75 80
Phe Val Thr Phe Cys Ala Phe Gln Asp Thr Ser Gln Gln Leu Ala Ala	85	90	95
Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu	100	105	110
Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser Pro Gly	115	120	125
Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu	130	135	140
Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Thr Ala Trp	145	150	155 160
Cys Leu His Trp Arg Arg Arg Arg Arg Arg Arg Ser Pro Tyr Pro Gly	165	170	175
Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro Glu Asp	180	185	190
Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu	195	200	205
Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro	210	215	220
Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro Leu Cys	225	230	235 240
Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile	245	250	

<210> 32

<211> 750

<212> DNA

<213> Canis familiaris

<400> 32

tatacaattt cttgggggca aggactttgt acagaggggg agaggtgggg ctggggctgg 60

ctttgggggc gttgggggag ggcgttgctt tgatcctggg gagggagcga gcggggctgc 120

gtggtcgagg aagggaccag tctctagctg actccctcca ggtcccagct ctgtgtcctc 180

gggcagatgg ctccgctcgc tgggcctcag tgtcctctgc tcccagggt agggtagacct 240

ccgccgccgc ctccttcgcc aatgcaggca ccaggcagtg gacatcagca ggagagccac 300

gggcagcagc agcaggagga gcagccgagg tgcttgaggg gctggcaagg cagtggcctc 360

cagggccccg gggctccttg ggggcaccaa ttagaggag tcgggctgac actgcagctc 420

caggcaccgc gagaaattcc tgcgggtgat ccagggttc agggcgcca gctgctggga 480

ggtgtcctgg aaggcacaga aggtgacaaa gtgtatctcc gtgttgacag cctccagcag 540

gatttgcat tgggatccag ccacagcctg gagccgcacc atccagcgt gggccaggac 600

caggcgccag aacgccccgc agagctcgtc gtctgcagg ttggaggcga cagtgactgg 660

atagtcctga agcaggtaat cagacagctt gcggatgggtg accgcgaagg tggaggagat 720

ggggctgtgg ctgaaggagc agtcgggggt 750

<210> 33

<211> 1019

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (74)..(166)

<400> 33

ccggcctggc cccttcacg ccagctggg gcaagcctga tctgaccata ggcagtaggg 60

gcctccggcc gag atg ata gtg ctg gcg cca gcc tgg agc cca act gtg 109

Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Val

1 5 10

cgt ata ccc ggg gga caa ggc ggg gga cag gca gag cgc tac cga gct 157

Arg Ile Pro Gly Gly Gln Gly Gly Gly Gln Ala Glu Arg Tyr Arg Ala

15

20

25

ggg cag agc tgagagagca gacggacaga ggcctccctg ttgctgctgc 206
 Gly Gln Ser
 30
 tgctgctcag ccccggcctc cgcgggaccc ccgactgctc cttcagccac agcccatct 266
 cctccacctt cgcggtcacc atccgcaagc tgtctgatta cctgcttcag gactatccag 326
 tcaactgtcg ctccaacctg caggacgacg agctctgcgg ggcgttctgg cgcctgggtcc 386
 tggcccagcg ctggatgggtg cggctccagg ctgtggctgg atcccaaag caaatcctgc 446
 tggaggctgt caacacggag atacactttg tcaccttctg tgccttcag gacacctccc 506
 agcagctggc cgcctgaag ccctggatca cccgcaggaa tttctccggg tgccctggagc 566
 tgcagtgtca gcccgactcc tctacattgg tgccccaag gagccccggg gccctggagg 626
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 ctctcctgct gatgtccact gcctgggtgcc tgcatggcg aaggaggcgg cggcggaggt 746
 caccctaccc tggggagcag aggacactga ggcccagcga gcggagccat ctgcccgagg 806
 acacagagct gggacctgga gggagtcagc tagagactgg tcccttcctc gaccacgcag 866
 ccccgctcgc tccctcccca ggatcaaggc aacgcccgcc cccaacgccc ccaaagccag 926
 cccagcccc acctctcccc ctctgtacaa agtccttgcc cccaagaaat tgtatataaa 986
 tcatacctttt ctaccaaaaa aaaaaaaaaa aaa 1019

<210> 34

<211> 31

<212> PRT

<213> Canis familiaris

<400> 34

Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Val Arg Ile Pro Gly
 1 5 10 15

Gly Gln Gly Gly Gly Gln Ala Glu Arg Tyr Arg Ala Gly Gln Ser
 20 25 30

<210> 35

<211> 1019

<212> DNA

<213> Canis familiaris

<400> 35

tttttttttt ttttttttgg tagaaaagga tgatttatat acaatttctt gggggcaagg 60
actttgtaca gagggggaga ggtggggctg gggctggctt tgggggcgtt gggggcgggc 120
gttgccctga tcctggggag ggagcgagcg gggctgcgtg gtcgaggaag ggaccagtct 180
ctagctgact ccctccaggt ccagctctg tgcctcggg cagatggctc cgctcgctgg 240
gcctcagtgt cctctgctcc ccagggtagg gtgacctcg ccgcgcctc ctcgccaat 300
gcaggcacca ggcagtggac atcagcagga gagccacggg cagcagcagc aggaggagca 360
gccgaggtgc ctgaggggct ggcaaggcag tggcctccag ggccccgggg ctcttgggg 420
gcaccaatgt agaggagtcg ggctgacact gcagctccag gcacccggag aaattcctgc 480
gggtgatcca gggcttcagg gcggccagct gctgggaggt gtcctggaag gcacagaagg 540
tgacaaagtg tatctccgtg ttgacagcct ccagcaggat ttgcatttg gatccagcca 600
cagcctggag ccgcaccatc cagcgctggg ccaggaccag gcgccagaac gccccgcaga 660
gctcgtcgtc ctgcaggttg gaggcgacag tgactggata gtcctgaagc aggtaatcag 720
acagcttgcg gatggtgacc gcgaaggctg aggagatggg gctgtggctg aaggagcagt 780
cggggggtccc gcggaggccg gggctgagca gcagcagcag caacagggag gcctctgtcc 840
gtctgctctc tcagctctgc ccagctcggg agcgctctgc ctgtcccccg ccttggtccc 900
cgggtatacg cacagttggg ctccaggctg gcgccagcac tatcatctcg gccggaggcc 960
cctcatgcct atggtcagat caggcttgcc ccagctgggc gtggaagggg ccaggccgg 1019

<210> 36

<211> 93

<212> DNA

<213> Canis familiaris

<400> 36

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ggacaggcag agcgctaccg agctgggcag agc

93

<210> 37

<211> 93

<212> DNA

<213> Canis familiaris

<400> 37

gctctgcca gctcggtagc gctctgcctg tccccgcct tgtccccgg gtatacgac 60

agttgggctc caggctggcg ccagcactat cat

93

<210> 38

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 38

tgaattcgga cataacttca atattac

27

<210> 39

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 39

tctcgagatt cagcttcaat gcctgta

27

<210> 40

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

Primer

<400> 40

cccaagctta tgggtctcac ctccaac

28

<210> 41

<211> 395

<212> DNA

<213> Felis catus

<400> 41

ggccataggc atgaagggcc tccggccgag atgatagtgc tggcgccagc ctggagccca 60

actacctccc tgctgctgct gctactgctc agccctggcc tccgcgggtc ccccgactgt 120

tccttcagcc acagcccccatt ctctccacc ttcaagggtca ccatccgaaa gctgtctgat 180

tacctgcttc aggattaccc agtcaccgtc gcctccaacc tacaggacga cgagctctgt 240

gggccattct ggcacctggc cctggcccag cgctggatgg gtcgggtcaa ggctgtggct 300

gggtcccaga tgcaaagcct gctggaggcg gtcaacaccg agatacattt tgtcaccttg 360

tgtgccttcc agcccctccc cagctgtctt cgatt 395

<210> 42

<211> 793

<212> DNA

<213> Felis catus

<400> 42

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cgccccaac ctacaggacg acgagctctg tgggccattc tggcacctgg tcctggccca 120

gcgctggatg ggtcgggtca aggctgtggc tgggtcccag atgcaaagcc tgctggaggc 180

ggtcaacacc gagatacatt ttgtcacctt gtgtgccttc cagcccctcc ccagctgtct 240

tcgattcgtc cagaccaaca tctcccacct cctgcaggac acctccgagc agctggcggc 300

cttgaagccc tggatcaccg gcaggaattt ctcggggtgc ctggagctac agtgtcagcc 360

cgactcctcc accccactgc cccaaggag cccagggcc ttggaggcca cagccctgcc 420

agcccctcag gcccctctgc tgctcctcct gctgctgttg cctgtggctc tcttgctgat 480

gtccgccgcc tgggtgcctgc actggcgaag aaggagatgg agaacgccct accccagggg 540
gcagaggaag aactgagggc ccagagagag gaatcacctg cccgaggaca cagagccggg 600
actcggagaa agtcagctag agactgggttc cttcctcgac cacgctgccc cgctcactct 660
ccccccggga tggaggcaac gccagcccc aacgccagcc ccagaccac ctatccccct 720
ctgtacaaag tccttgtcct caggaaattg tatataaatc atccttttct accaaaaaaaa 780
aaaaaaaaaa aaa 793

<210> 43
<211> 942
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (31)..(903)

<400> 43
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Met Ile Val Leu Ala Pro Ala Trp
1 5
agc cca act acc tcc ctg ctg ctg ctg cta ctg ctc agc cct ggc ctc 102
Ser Pro Thr Thr Ser Leu Leu Leu Leu Leu Leu Ser Pro Gly Leu
10 15 20
cgc ggg tcc ccc gac tgt tcc ttc agc cac agc ccc atc tcc tcc acc 150
Arg Gly Ser Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr
25 30 35 40
ttc aag gtc acc atc cga aag ctg tct gat tac ctg ctt cag gat tac 198
Phe Lys Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr
45 50 55
cca gtc acc gtc gcc tcc aac cta cag gac gac gag ctc tgt ggg cca 246
Pro Val Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Pro
60 65 70
ttc tgg cac ctg gtc ctg gcc cag cgc tgg atg ggt cgg ctc aag gct 294
Phe Trp His Leu Val Leu Ala Gln Arg Trp Met Gly Arg Leu Lys Ala
75 80 85

gtg gct ggg tcc cag atg caa agc ctg ctg gag gcg gtc aac acc gag 342
 Val Ala Gly Ser Gln Met Gln Ser Leu Leu Glu Ala Val Asn Thr Glu
 90 95 100

ata cat ttt gtc acc ttg tgt gcc ttc cag ccc ctc ccc agc tgt ctt 390
 Ile His Phe Val Thr Leu Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu
 105 110 115 120

cga ttc gtc cag acc aac atc tcc cac ctc ctg cag gac acc tcc gag 438
 Arg Phe Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Glu
 125 130 135

cag ctg gcg gcc ttg aag ccc tgg atc acc cgc agg aat ttc tcg ggg 486
 Gln Leu Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly
 140 145 150

tgc ctg gag cta cag tgt cag ccc gac tcc tcc acc cca ctg ccc cca 534
 Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Pro Leu Pro Pro
 155 160 165

agg agc ccc agg gcc ttg gag gcc aca gcc ctg cca gcc cct cag gcc 582
 Arg Ser Pro Arg Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala
 170 175 180

cct ctg ctg ctc ctc ctg ctg ctg ttg cct gtg gct ctc ttg ctg atg 630
 Pro Leu Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met
 185 190 195 200

tcc gcc gcc tgg tgc ctg cac tgg cga aga agg aga tgg aga acg ccc 678
 Ser Ala Ala Trp Cys Leu His Trp Arg Arg Arg Arg Trp Arg Thr Pro
 205 210 215

tac ccc agg gag cag agg aag aca ctg agg ccc aga gag agg aat cac 726
 Tyr Pro Arg Glu Gln Arg Lys Thr Leu Arg Pro Arg Glu Arg Asn His
 220 225 230

ctg ccc gag gac aca gag ccg gga ctc gga gaa agt cag cta gag act 774
 Leu Pro Glu Asp Thr Glu Pro Gly Leu Gly Glu Ser Gln Leu Glu Thr
 235 240 245

ggt tcc ttc ctc gac cac gct gcc ccg ctc act ctc ccc ccg gga tgg 822
 Gly Ser Phe Leu Asp His Ala Ala Pro Leu Thr Leu Pro Pro Gly Trp
 250 255 260

agg caa cgc cag ccc cca acg cca gcc cca gac cca cct atc ccc ctc 870
 Arg Gln Arg Gln Pro Pro Thr Pro Ala Pro Asp Pro Pro Ile Pro Leu
 265 270 275 280

tgt aca aag tcc ttg tcc tca gga aat tgt ata taaatcatcc ttttctacca 923
 Cys Thr Lys Ser Leu Ser Ser Gly Asn Cys Ile
 285 290

aaaaaaaaa aaaaaaaaaa

942

<210> 44

<211> 291

<212> PRT

<213> Felis catus

<400> 44

Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Ser Leu Leu Leu
 1 5 10 15

Leu Leu Leu Leu Ser Pro Gly Leu Arg Gly Ser Pro Asp Cys Ser Phe
 20 25 30

Ser His Ser Pro Ile Ser Ser Thr Phe Lys Val Thr Ile Arg Lys Leu
 35 40 45

Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
 50 55 60

Gln Asp Asp Glu Leu Cys Gly Pro Phe Trp His Leu Val Leu Ala Gln
 65 70 75 80

Arg Trp Met Gly Arg Leu Lys Ala Val Ala Gly Ser Gln Met Gln Ser
 85 90 95

Leu Leu Glu Ala Val Asn Thr Glu Ile His Phe Val Thr Leu Cys Ala
 100 105 110

Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 115 120 125

His Leu Leu Gln Asp Thr Ser Glu Gln Leu Ala Ala Leu Lys Pro Trp
 130 135 140

Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu Gln Cys Gln Pro
 145 150 155 160

Asp Ser Ser Thr Pro Leu Pro Pro Arg Ser Pro Arg Ala Leu Glu Ala
 165 170 175

Thr Ala Leu Pro Ala Pro Gln Ala Pro Leu Leu Leu Leu Leu Leu
 180 185 190

Leu Pro Val Ala Leu Leu Leu Met Ser Ala Ala Trp Cys Leu His Trp
 195 200 205

Arg Arg Arg Arg Trp Arg Thr Pro Tyr Pro Arg Glu Gln Arg Lys Thr
 210 215 220

Leu Arg Pro Arg Glu Arg Asn His Leu Pro Glu Asp Thr Glu Pro Gly
 225 230 235 240

Leu Gly Glu Ser Gln Leu Glu Thr Gly Ser Phe Leu Asp His Ala Ala
 245 250 255

Pro Leu Thr Leu Pro Pro Gly Trp Arg Gln Arg Gln Pro Pro Thr Pro
 260 265 270

Ala Pro Asp Pro Pro Ile Pro Leu Cys Thr Lys Ser Leu Ser Ser Gly
 275 280 285

Asn Cys Ile
 290

<210> 45

<211> 942

<212> DNA

<213> *Felis catus*

<400> 45

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ggactttgta cagaggggga taggtgggtc tggggctggc gttgggggct ggcgttgcct 120

ccatcccggg gggagagtga gcggggcagc gtggctcagg aaggaaccag tctctagctg 180

actttctccg agtcccggct ctgtgtcctc gggcaggtga ttctctctc tgggcctcag 240

tgtcttctc tgctccctgg ggtagggcgt tctccatctc cttcttcgcc agtgcaggca 300

ccaggcggcg gacatcagca agagagccac aggcaacagc agcaggagga gcagcagagg 360

ggcctgaggg gctggcaggg ctgtggcctc caaggccctg gggctccttg ggggcagtgg 420

ggtggaggag tcgggctgac actgtagctc caggcaccac gagaaattcc tgcgggtgat 480

ccagggcttc aaggccgcca gctgctcgga ggtgtcctgc aggaggtggg agatgttggt 540

ctggacgaat cgaagacagc tggggagggg ctggaaggca cacaaggtga caaatgtat 600

ctcgggtgttg accgcctcca gcaggctttg catctgggac ccagccacag ccttgagccg 660
acccatccag cgctgggcca ggaccaggtg ccagaatggc ccacagagct cgtcgtcctg 720
taggttggag gcgacggtga ctgggtaatc ctgaagcagg taatcagaca gctttcggat 780
ggtgaccttg aaggtggagg agatggggct gtggctgaag gaacagtcgg gggacccgcg 840
gaggccaggg ctgagcagta gcagcagcag cagggaggta gttgggctcc aggctggcgc 900
cagcactatc atctcggccg gaggcccttc atgcctatgg cc 942

<210> 46

<211> 873

<212> DNA

<213> Felis catus

<400> 46

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agccctggcc tccgcgggtc ccccgactgt tccttcagcc acagcccat ctcctccacc 120
ttcaagggtca ccatccgaaa gctgtctgat tacctgcttc aggattaccc agtcaccgtc 180
gcctccaacc tacaggacga cgagctctgt gggccattct ggcacctggt cctggcccag 240
cgctggatgg gtcgggtcaa ggctgtggct gggteccaga tgcaaagcct gctggaggcg 300
gtcaacaccg agatacattt tgtcaccttg tgtgccttcc agccctccc cagctgtctt 360
cgattcgtcc agaccaacat ctcccacctc ctgcaggaca cctccgagca gctggcggcc 420
ttgaagccct ggatcacccg caggaatttc tcggggtgcc tggagctaca gtgtcagccc 480
gactcctcca cccactgcc cccaaggagc ccaggggcct tggaggccac agccctgcca 540
gcccctcagg cccctctgct gctcctcctg ctgctgttgc ctgtggctct cttgctgatg 600
tccgccgcct ggtgcctgca ctggcgaaga aggagatgga gaacgcccta cccagggag 660
cagaggaaga cactgaggcc cagagagagg aatcacctgc ccgaggacac agagccggga 720
ctcggagaaa gtcagctaga gactggttcc ttctcagacc acgctgcccc gctcactctc 780
cccccgggat ggaggcaacg ccagcccccac acgccagccc cagaccacc tatccccctc 840

tgcacaaagt ccttgctctc aggaaattgt ata

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<210> 47

<211> 873

<212> DNA

<213> Felis catus

<400> 47

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cgttgggggc tggcgttgcc tccatcccgg ggggagagtg agcggggcag cgtggtcgag 120
gaaggaacca gtctctagct gactttctcc gagtcccggc tctgtgtcct cgggcaggtg 180
attcctctct ctgggectca gtgtcttctt ctgtccctg gggtagggcg ttctccatct 240
ccttcttcgc cagtgcaggc accaggcggc ggacatcagc aagagagcca caggcaacag 300
cagcaggagg agcagcagag gggcctgagg ggctggcagg gctgtggcct ccaaggccct 360
ggggctcctt gggggcagtg gggtaggagga gtcgggctga cactgtagct ccaggcaccc 420
cgagaaattc ctgcgggtga tccagggtt caaggccgcc agctgtcgg aggtgtcctg 480
caggaggtgg gagatgttgg tctggacgaa tcgaagacag ctggggaggg gctggaaggc 540
acacaaggtg acaaaatgta tctcgggtgt gaccgectcc agcaggcttt gcatctggga 600
cccagccaca gccttgagcc gacccatcca gcgctgggcc aggaccaggt gccagaatgg 660
cccacagagc tcgtcgtcct gtaggttgga ggcgacggtg actgggtaat cctgaagcag 720
gtaatcagac agctttcggg tggtagcctt gaaggtggag gagatggggc tgtggctgaa 780
ggaacagtcg ggggacccgc ggaggccagg gctgagcagt agcagcagca gcagggaggt 840
agttgggctc caggctggcg ccagcactat cat 873

<210> 48

<211> 795

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1) .. (795)

<400> 48

tcc ccc gac tgt tcc ttc agc cac agc ccc atc tcc tcc acc ttc aag	48
Ser Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Lys	
1 5 10 15	
gtc acc atc cga aag ctg tct gat tac ctg ctt cag gat tac cca gtc	96
Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val	
20 25 30	
acc gtc gcc tcc aac cta cag gac gac gag ctc tgt ggg cca ttc tgg	144
Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Pro Phe Trp	
35 40 45	
cac ctg gtc ctg gcc cag cgc tgg atg ggt cgg ctc aag gct gtg gct	192
His Leu Val Leu Ala Gln Arg Trp Met Gly Arg Leu Lys Ala Val Ala	
50 55 60	
ggg tcc cag atg caa agc ctg ctg gag gcg gtc aac acc gag ata cat	240
Gly Ser Gln Met Gln Ser Leu Leu Glu Ala Val Asn Thr Glu Ile His	
65 70 75 80	
ttt gtc acc ttg tgt gcc ttc cag ccc ctc ccc agc tgt ctt cga ttc	288
Phe Val Thr Leu Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe	
85 90 95	
gtc cag acc aac atc tcc cac ctc ctg cag gac acc tcc gag cag ctg	336
Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Glu Gln Leu	
100 105 110	
gcg gcc ttg aag ccc tgg atc acc cgc agg aat ttc tcg ggg tgc ctg	384
Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu	
115 120 125	
gag cta cag tgt cag ccc gac tcc tcc acc cca ctg ccc cca agg agc	432
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Pro Leu Pro Pro Arg Ser	
130 135 140	
ccc agg gcc ttg gag gcc aca gcc ctg cca gcc cct cag gcc cct ctg	480
Pro Arg Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Leu	
145 150 155 160	
ctg ctc ctc ctg ctg ctg ttg cct gtg gct ctc ttg ctg atg tcc gcc	528
Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Ala	
165 170 175	
gcc tgg tgc ctg cac tgg cga aga agg aga tgg aga acg ccc tac ccc	576
Ala Trp Cys Leu His Trp Arg Arg Arg Arg Trp Arg Thr Pro Tyr Pro	

180 185 190
 agg gag cag agg aag aca ctg agg ccc aga gag agg aat cac ctg ccc 624
 Arg Glu Gln Arg Lys Thr Leu Arg Pro Arg Glu Arg Asn His Leu Pro
 195 200 205
 gag gac aca gag ccg gga ctc gga gaa agt cag cta gag act ggt tcc 672
 Glu Asp Thr Glu Pro Gly Leu Gly Glu Ser Gln Leu Glu Thr Gly Ser
 210 215 220
 ttc ctc gac cac gct gcc ccg ctc act ctc ccc ccg gga tgg agg caa 720
 Phe Leu Asp His Ala Ala Pro Leu Thr Leu Pro Pro Gly Trp Arg Gln
 225 230 235 240
 cgc cag ccc cca acg cca gcc cca gac cca cct atc ccc ctc tgt aca 768
 Arg Gln Pro Pro Thr Pro Ala Pro Asp Pro Pro Ile Pro Leu Cys Thr
 245 250 255
 aag tcc ttg tcc tca gga aat tgt ata 795
 Lys Ser Leu Ser Ser Gly Asn Cys Ile
 260 265

<210> 49
 <211> 265
 <212> PRT
 <213> Felis catus

<400> 49
 Ser Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Lys
 1 5 10 15
 Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val
 20 25 30
 Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Pro Phe Trp
 35 40 45
 His Leu Val Leu Ala Gln Arg Trp Met Gly Arg Leu Lys Ala Val Ala
 50 55 60
 Gly Ser Gln Met Gln Ser Leu Leu Glu Ala Val Asn Thr Glu Ile His
 65 70 75 80
 Phe Val Thr Leu Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe
 85 90 95
 Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Glu Gln Leu

100 105 110
Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu
115 120 125
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Pro Leu Pro Pro Arg Ser
130 135 140
Pro Arg Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Leu
145 150 155 160
Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Ala
165 170 175
Ala Trp Cys Leu His Trp Arg Arg Arg Arg Trp Arg Thr Pro Tyr Pro
180 185 190
Arg Glu Gln Arg Lys Thr Leu Arg Pro Arg Glu Arg Asn His Leu Pro
195 200 205
Glu Asp Thr Glu Pro Gly Leu Gly Glu Ser Gln Leu Glu Thr Gly Ser
210 215 220
Phe Leu Asp His Ala Ala Pro Leu Thr Leu Pro Pro Gly Trp Arg Gln
225 230 235 240
Arg Gln Pro Pro Thr Pro Ala Pro Asp Pro Pro Ile Pro Leu Cys Thr
245 250 255
Lys Ser Leu Ser Ser Gly Asn Cys Ile
260 265

<210> 50

<211> 795

<212> DNA

<213> Felis catus

<400> 50

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cgttgggggc tggcgttgcc tccatcccgg ggggagagtg agcggggcag cgtggtcgag 120
gaaggaacca gtctctagct gactttctcc gagtcccggc tctgtgtcct cgggcaggtg 180
attcctctct ctgggcctca gtgtcttcct ctgctccctg gggtagggcg ttctccatct 240
ccttcttcgc cagtgcaggc accaggcggc ggacatcagc aagagagcca caggcaacag 300

cagcaggagg agcagcagag gggcctgagg ggctggcagg gctgtggcct ccaaggccct 360
 ggggctcctt gggggcagtg ggggtggagga gtcgggctga cactgtagct ccaggcaccc 420
 cgagaaattc ctgcgggtga tccagggctt caaggccgcc agctgctcgg aggtgtcctg 480
 caggaggtgg gagatgttgg tctggacgaa tcgaagacag ctggggaggg gctggaaggc 540
 acacaagggtg acaaaatgta tctcgggtgtt gaccgcctcc agcaggcttt gcatctggga 600
 cccagccaca gccttgagcc gacccatcca gcgctgggcc aggaccaggt gccagaatgg 660
 cccacagagc tcgtcgtcct gtaggttgga ggcgacggtg actgggtaat cctgaagcag 720
 gtaatcagac agcttttcgga tggtgacctt gaaggtggag gagatggggc tgtggctgaa 780
 ggaacagtcg gggga 795

<210> 51
 <211> 321
 <212> DNA
 <213> Canis familiaris

<400> 51
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 gtgaagggttc aggcggggaac taacaagact gatgttatct gtgggtcccca gcctcgggtta 120
 agagccctag tgggtgggtccc catcattatg gggatcctgc ttgttgcct gttggtgtct 180
 gcctgcatcc gaaagggtgg caagaagcca gagaataagg ttatgtatca ggaccctgtg 240
 gaggacttgg aggaatttcc tatgcccccg cactccattg ctccggtgca agagacctta 300
 catgggtgcc agcccgtcac c 321

<210> 52
 <211> 1425
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (196)..(1017)

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tgcccaacga agccggccac gattggtccc cgaagacccc gcccatctcc tgggcggggc 120

gggcgggggc aagggtctggg gagttactaa agacatcccc gcgcccctac tccgctgcct 180

gctattcacc tcgcc atg gtt ctc ctg cct ctg cgc tgt ctc ttc tgg ggc 231

Met Val Leu Leu Pro Leu Arg Cys Leu Phe Trp Gly

1

5

10

tcc ttg ttg acc acc gtc tac cca gaa cca cgc act gca tgc aga gaa 279

Ser Leu Leu Thr Thr Val Tyr Pro Glu Pro Arg Thr Ala Cys Arg Glu

15

20

25

aag caa tac cta gta gac agt cag tgc tgt aat atg tgc cca cca gga 327

Lys Gln Tyr Leu Val Asp Ser Gln Cys Cys Asn Met Cys Pro Pro Gly

30

35

40

gag aaa ctg gtg aat gac tgc cta cat acc att gac acg gaa tgc act 375

Glu Lys Leu Val Asn Asp Cys Leu His Thr Ile Asp Thr Glu Cys Thr

45

50

55

60

cgt tgc caa aca ggc gaa ttc cta gac act tgg aac gca gag aga cac 423

Arg Cys Gln Thr Gly Glu Phe Leu Asp Thr Trp Asn Ala Glu Arg His

65

70

75

tgt cac cag cac aaa tac tgc gac ccc aac cta ggg ctc cat gtc gag 471

Cys His Gln His Lys Tyr Cys Asp Pro Asn Leu Gly Leu His Val Glu

80

85

90

aag gag ggc acg tca gaa aca gac acc act tgc aca tgc gat gaa ggt 519

Lys Glu Gly Thr Ser Glu Thr Asp Thr Thr Cys Thr Cys Asp Glu Gly

95

100

105

ctg cat tgt acc aac gct gcc tgt gag agc tgc acc atg cac agc ctg 567

Leu His Cys Thr Asn Ala Ala Cys Glu Ser Cys Thr Met His Ser Leu

110

115

120

tgc ccc cct ggc ctg gga gtc aaa cag atc gct aca ggg att tct gat 615

Cys Pro Pro Gly Leu Gly Val Lys Gln Ile Ala Thr Gly Ile Ser Asp

125

130

135

140

acc atc tgc gat ccc tgc ccc atc ggc ttc ttc tcc aat gtg tct tct 663

Thr Ile Cys Asp Pro Cys Pro Ile Gly Phe Phe Ser Asn Val Ser Ser

145

150

155

gct ttg gaa aag tgt cac cct tgg aca agc tgt gaa acc aaa ggc ctg 711

Ala Leu Glu Lys Cys His Pro Trp Thr Ser Cys Glu Thr Lys Gly Leu
 160 165 170

gtg aag gtt cag gcg gga act aac aag act gat gtt atc tgt ggt ccc 759
 Val Lys Val Gln Ala Gly Thr Asn Lys Thr Asp Val Ile Cys Gly Pro
 175 180 185

cag cct cgg tta aga gcc cta gtg gtg gtc ccc atc att atg ggg atc 807
 Gln Pro Arg Leu Arg Ala Leu Val Val Val Pro Ile Ile Met Gly Ile
 190 195 200

ctg ctt gtt gtc ctg ttg gtg tct gcc tgc atc cga aag gtg gtc aag 855
 Leu Leu Val Val Leu Leu Val Ser Ala Cys Ile Arg Lys Val Val Lys
 205 210 215 220

aag cca gag aat aag gtt atg tat cag gac cct gtg gag gac ttg gag 903
 Lys Pro Glu Asn Lys Val Met Tyr Gln Asp Pro Val Glu Asp Leu Glu
 225 230 235

gaa ttt cct atg ccc ccg cac tcc att gct ccg gtg caa gag acc tta 951
 Glu Phe Pro Met Pro Pro His Ser Ile Ala Pro Val Gln Glu Thr Leu
 240 245 250

cat ggg tgc cag ccc gtc acc cag gag gac ggc aaa gag agc cgc atc 999
 His Gly Cys Gln Pro Val Thr Gln Glu Asp Gly Lys Glu Ser Arg Ile
 255 260 265

tcc gtg cag gag aga gtg tgaggcagcg tgtgcccagg agtgtgacag 1047
 Ser Val Gln Glu Arg Val
 270

cgtgggagag tgggcgcgtg gctggagagc ctggagctgc tggagggggca tgaagggggcg 1107

gtgctcccct gcctgcaccc ctgtgctgca gaaacagaga accttccacc ccacccttg 1167

agcccattcc acctcccaac ttgcttttaa agatggagat gaaacttttg gggggccaga 1227

tagtaatatc caccaaccca gcatttcagg gccctgaggt gtatatcacg gtggtttcta 1287

cgagcccagg aagaccacg aagagccatt gtggcattgt ttgtgacagt ggacaactgg 1347

aggccactta gctgttcagc agcaggggac tggctaaata aaatttgtaa tatatttata 1407

aaaaaaaaa aaaaaaaaaa 1425

<210> 53

<211> 274

<212> PRT

<213> Canis familiaris

<400> 53

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Met Val Leu Leu Pro Leu Arg Cys Leu Phe Trp Gly Ser Leu Leu Thr
  1             5             10             15

Thr Val Tyr Pro Glu Pro Arg Thr Ala Cys Arg Glu Lys Gln Tyr Leu
      20             25             30

Val Asp Ser Gln Cys Cys Asn Met Cys Pro Pro Gly Glu Lys Leu Val
      35             40             45

Asn Asp Cys Leu His Thr Ile Asp Thr Glu Cys Thr Arg Cys Gln Thr
      50             55             60

Gly Glu Phe Leu Asp Thr Trp Asn Ala Glu Arg His Cys His Gln His
      65             70             75             80

Lys Tyr Cys Asp Pro Asn Leu Gly Leu His Val Glu Lys Glu Gly Thr
      85             90             95

Ser Glu Thr Asp Thr Thr Cys Thr Cys Asp Glu Gly Leu His Cys Thr
      100            105            110

Asn Ala Ala Cys Glu Ser Cys Thr Met His Ser Leu Cys Pro Pro Gly
      115            120            125

Leu Gly Val Lys Gln Ile Ala Thr Gly Ile Ser Asp Thr Ile Cys Asp
      130            135            140

Pro Cys Pro Ile Gly Phe Phe Ser Asn Val Ser Ser Ala Leu Glu Lys
      145            150            155            160

Cys His Pro Trp Thr Ser Cys Glu Thr Lys Gly Leu Val Lys Val Gln
      165            170            175

Ala Gly Thr Asn Lys Thr Asp Val Ile Cys Gly Pro Gln Pro Arg Leu
      180            185            190

Arg Ala Leu Val Val Val Pro Ile Ile Met Gly Ile Leu Leu Val Val
      195            200            205

Leu Leu Val Ser Ala Cys Ile Arg Lys Val Val Lys Lys Pro Glu Asn
      210            215            220

Lys Val Met Tyr Gln Asp Pro Val Glu Asp Leu Glu Glu Phe Pro Met
      225            230            235            240

```

Pro Pro His Ser Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln
 245 250 255

Pro Val Thr Gln Glu Asp Gly Lys Glu Ser Arg Ile Ser Val Gln Glu
 260 265 270

Arg Val

<210> 54

<211> 1425

<212> DNA

<213> Canis familiaris

<400> 54

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 tgggtcttcc tgggctcgta gaaaccaccg tgatatacac ctccaggccc tgaaatgctg 180
 gggttggtgga tattactatc tggcccccca aaagtttcat ctccatcttt aaaagcaagt 240
 tgggaggtgg aatgggctcc aggggtgggg tggaaggttc tctgtttctg cagcacaggg 300
 gtgcaggcag gggagcaccg ccccttcatg cccctccagc agctccaggc tctccagcca 360
 cgcgcccact ctcccacgct gtcacactcc tgggcacacg ctgcctcaca ctctctcctg 420
 cacggagatg cggtctcttt tgccgtcctc ctgggtgacg ggctggcacc catgtaaggt 480
 ctcttgacc ggagcaatgg agtgcggggg cataggaaat tctccaagt cctccacagg 540
 gtctgatac ataaccttat tctctggctt cttgaccacc tttcggatgc aggcagacac 600
 caacaggaca acaagcagga tccccataat gatggggacc accactaggg ctcttaaccg 660
 aggctgggga ccacagataa catcagtctt gttagttccc gcctgaacct tcaccaggcc 720
 tttggtttca cagcttgtcc aagggtgaca cttttccaaa gcagaagaca cattggagaa 780
 gaagccgatg gggcagggat cgcagatggt atcagaaatc cctgtagcga tctgtttgac 840
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atggagccct aggttgggggt cgcagtatTT gtgctggtga cagtgtctct ctgcgttcca 1020
agtgtctagg aattcgccctg ttTggcaacg agtgcattcc gtgtcaatgg tatgtaggca 1080
gtcattcacc agtttctctc ctggTgggca catattacag cactgactgt ctactaggta 1140
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gaagagacag cgcagaggca ggagaaccat ggcgaggTga atagcaggca gcggagtagg 1260
ggcgcgggga tgtcttttagt aactccccag cccttgcccc cgcccgcccc gcccaggaga 1320
tgggcggggT cttcggggac caatcgtggc cggttcgtt gggcagggcg gagctcctgg 1380
agacccttag cgccgggagT tccctgaat attcccgga gtcta 1425

<210> 55

<211> 822

<212> DNA

<213> Canis familiaris

<400> 55

atggttctcc tgcctctgcg ctgtctcttc tggggctcct tgttgaccac cgtctacca 60
gaaccaogca ctgcatgcag agaaaagcaa tacctagtag acagtcagtg ctgtaatatg 120
tgcccaccag gagagaaact ggtgaatgac tgcctacata ccattgacac ggaatgcact 180
cgttgccaaa caggcgaatt cctagacact tggaacgcag agagacactg tcaccagcac 240
aaatactgcg accccaacct agggctccat gtcgagaagg agggcacgtc agaaacagac 300
accacttgca catgcgatga aggtctgcat tgtaccaacg ctgcctgtga gagctgcacc 360
atgcacagcc tgtgcccccc tggcctggga gtcaaacaga tcgctacagg gatttctgat 420
accatctgcg atccctgccc catcggtctc ttctccaatg tgtcttctgc ttTggaaaag 480
tgtcaccctt ggacaagctg tgaaaccaaa ggctggtga aggttcaggc gggaactaac 540
aagactgatg ttatctgtgg tccccagcct cggttaagag ccctagtggT ggtccccatc 600
attatgggga tcctgcttgt tgtcctgttg gtgtctgcct gcatccgaaa ggtggTcaag 660
aagccagaga ataaggttat gtatcaggac cctgtggagg acttgaggga atttcctatg 720

ccccgcact ccattgctcc ggtgcaagag accttacatg ggtgccagcc cgtcacccag 780
gaggacggca aagagagccg catctccgtg caggagagag tg 822

<210> 56
<211> 822
<212> DNA
<213> Canis familiaris

<400> 56
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cccatgtaag gtctcttgca ccggagcaat ggagtgcggg ggcataggaa attcctccaa 120
gtcctccaca gggtcctgat acataacctt attctctggc ttcttgacca cctttcggat 180
gcaggcagac accaacagga caacaagcag gatccccata atgatgggga ccaccactag 240
ggctcttaac cgaggctggg gaccacagat aacatcagtc ttgttagttc ccgcctgaac 300
cttcaccagg cctttggttt cacagcttgt ccaaggggtga cacttttcca aagcagaaga 360
cacattggag aagaagccga tggggcaggg atcgcagatg gtatcagaaa tcctgttagc 420
gatctgtttg actcccaggc caggggggca caggctgtgc atgggtgcagc tctcacaggc 480
agcgttggtg caatgcagac cttcatcgca tgtgcaagtg gtgtctgttt ctgacgtgcc 540
ctccttctcg acatggagcc ctaggttggg gtcgcagtat ttgtgctggt gacagtgtct 600
ctctgcgttc caagtgtcta ggaattcgcc tgtttggcaa cgagtgcatt ccgtgtcaat 660
ggtatgtagg cagtcattca ccagtttctc tcctgggtggg cacatattac agcactgact 720
gtctactagg tattgctttt ctctgcatgc agtgcgtggt tctgggtaga cggtggtcaa 780
caaggagccc cagaagagac agcgcagagg caggagaacc at 822

<210> 57
<211> 765
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(765)

<400> 57

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Pro Glu Pro Arg Thr Ala Cys Arg Glu Lys Gln Tyr Leu Val Asp Ser
  1             5             10             15

cag tgc tgt aat atg tgc cca cca gga gag aaa ctg gtg aat gac tgc      96
Gln Cys Cys Asn Met Cys Pro Pro Gly Glu Lys Leu Val Asn Asp Cys
          20             25             30

cta cat acc att gac acg gaa tgc act cgt tgc caa aca ggc gaa ttc      144
Leu His Thr Ile Asp Thr Glu Cys Thr Arg Cys Gln Thr Gly Glu Phe
          35             40             45

cta gac act tgg aac gca gag aga cac tgt cac cag cac aaa tac tgc      192
Leu Asp Thr Trp Asn Ala Glu Arg His Cys His Gln His Lys Tyr Cys
          50             55             60

gac ccc aac cta ggg ctc cat gtc gag aag gag ggc acg tca gaa aca      240
Asp Pro Asn Leu Gly Leu His Val Glu Lys Glu Gly Thr Ser Glu Thr
          65             70             75             80

gac acc act tgc aca tgc gat gaa ggt ctg cat tgt acc aac gct gcc      288
Asp Thr Thr Cys Thr Cys Asp Glu Gly Leu His Cys Thr Asn Ala Ala
          85             90             95

tgt gag agc tgc acc atg cac agc ctg tgc ccc cct ggc ctg gga gtc      336
Cys Glu Ser Cys Thr Met His Ser Leu Cys Pro Pro Gly Leu Gly Val
          100             105             110

aaa cag atc gct aca ggg att tct gat acc atc tgc gat ccc tgc ccc      384
Lys Gln Ile Ala Thr Gly Ile Ser Asp Thr Ile Cys Asp Pro Cys Pro
          115             120             125

atc ggc ttc ttc tcc aat gtg tct tct gct ttg gaa aag tgt cac cct      432
Ile Gly Phe Phe Ser Asn Val Ser Ser Ala Leu Glu Lys Cys His Pro
          130             135             140

tgg aca agc tgt gaa acc aaa ggc ctg gtg aag gtt cag gcg gga act      480
Trp Thr Ser Cys Glu Thr Lys Gly Leu Val Lys Val Gln Ala Gly Thr
          145             150             155             160

aac aag act gat gtt atc tgt ggt ccc cag cct cgg tta aga gcc cta      528
Asn Lys Thr Asp Val Ile Cys Gly Pro Gln Pro Arg Leu Arg Ala Leu
          165             170             175

gtg gtg gtc ccc atc att atg ggg atc ctg ctt gtt gtc ctg ttg gtg      576
Val Val Val Pro Ile Ile Met Gly Ile Leu Leu Val Val Leu Leu Val

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180	185	190	
tct gcc tgc atc cga aag gtg gtc aag aag cca gag aat aag gtt atg			624
Ser Ala Cys Ile Arg Lys Val Val Lys Lys Pro Glu Asn Lys Val Met			
195	200	205	
tat cag gac cct gtg gag gac ttg gag gaa ttt cct atg ccc ccg cac			672
Tyr Gln Asp Pro Val Glu Asp Leu Glu Glu Phe Pro Met Pro Pro His			
210	215	220	
tcc att gct ccg gtg caa gag acc tta cat ggg tgc cag ccc gtc acc			720
Ser Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln Pro Val Thr			
225	230	235	240
cag gag gac ggc aaa gag agc cgc atc tcc gtg cag gag aga gtg			765
Gln Glu Asp Gly Lys Glu Ser Arg Ile Ser Val Gln Glu Arg Val			
245	250	255	

<210> 58

<211> 255

<212> PRT

<213> Canis familiaris

<400> 58

Pro	Glu	Pro	Arg	Thr	Ala	Cys	Arg	Glu	Lys	Gln	Tyr	Leu	Val	Asp	Ser
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Gln	Cys	Cys	Asn	Met	Cys	Pro	Pro	Gly	Glu	Lys	Leu	Val	Asn	Asp	Cys
			20					25					30		

Leu	His	Thr	Ile	Asp	Thr	Glu	Cys	Thr	Arg	Cys	Gln	Thr	Gly	Glu	Phe
	35						40					45			

Leu	Asp	Thr	Trp	Asn	Ala	Glu	Arg	His	Cys	His	Gln	His	Lys	Tyr	Cys
	50						55				60				

Asp	Pro	Asn	Leu	Gly	Leu	His	Val	Glu	Lys	Glu	Gly	Thr	Ser	Glu	Thr
	65				70					75				80	

Asp	Thr	Thr	Cys	Thr	Cys	Asp	Glu	Gly	Leu	His	Cys	Thr	Asn	Ala	Ala
			85						90					95	

Cys	Glu	Ser	Cys	Thr	Met	His	Ser	Leu	Cys	Pro	Pro	Gly	Leu	Gly	Val
			100						105				110		

Lys	Gln	Ile	Ala	Thr	Gly	Ile	Ser	Asp	Thr	Ile	Cys	Asp	Pro	Cys	Pro
	115						120					125			

Ile Gly Phe Phe Ser Asn Val Ser Ser Ala Leu Glu Lys Cys His Pro
 130 135 140
 Trp Thr Ser Cys Glu Thr Lys Gly Leu Val Lys Val Gln Ala Gly Thr
 145 150 155 160
 Asn Lys Thr Asp Val Ile Cys Gly Pro Gln Pro Arg Leu Arg Ala Leu
 165 170 175
 Val Val Val Pro Ile Ile Met Gly Ile Leu Leu Val Val Leu Leu Val
 180 185 190
 Ser Ala Cys Ile Arg Lys Val Val Lys Lys Pro Glu Asn Lys Val Met
 195 200 205
 Tyr Gln Asp Pro Val Glu Asp Leu Glu Glu Phe Pro Met Pro Pro His
 210 215 220
 Ser Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln Pro Val Thr
 225 230 235 240
 Gln Glu Asp Gly Lys Glu Ser Arg Ile Ser Val Gln Glu Arg Val
 245 250 255

<210> 59

<211> 765

<212> DNA

<213> Canis familiaris

<400> 59

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 gtctccaca gggctctgat acataacctt attctctggc ttcttgacca cctttcggat 180
 gcaggcagac accaacagga caacaagcag gatccccata atgatgggga ccaccactag 240
 ggctcttaac cgaggctggg gaccacagat aacatcagtc ttgttagttc ccgcctgaac 300
 cttcaccagg cctttgggtt cacagcttgt ccaagggtga cacttttcca aagcagaaga 360
 cacattggag aagaagccga tggggcaggg atcgagatg gtatcagaaa tcctgtagc 420
 gatctgtttg actcccaggc caggggggca caggctgtgc atggtgcagc tctcacaggc 480

agcgttggtta caatgcagac cttcatcgca tgtgcaagtg gtgtctgttt ctgacgtgcc 540
 ctecttctcg acatggagcc ctaggttggg gtcgcagtat ttgtgctggg gacagtgtct 600
 ctctgcgttc caagtgtcta ggaattcgcc tgtttggtgcaa cgagtgcatt ccgtgtcaat 660
 ggtatgtagg cagtcattca ccagtttctc tcttggtggg cacatattac agcactgact 720
 gtctactagg tattgctttt ctctgcatgc agtgcggtgg tctgg 765

<210> 60

<211> 336

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(336)

<400> 60

aat gtg tca tct gct tcg gaa aag tgt cac cct tgg acg agg tgt gag 48
 Asn Val Ser Ser Ala Ser Glu Lys Cys His Pro Trp Thr Arg Cys Glu
 1 5 10 15

acc aaa ggc ctg gtg gag ctt cag gcg ggg acc aac aag acg gat gcc 96
 Thr Lys Gly Leu Val Glu Leu Gln Ala Gly Thr Asn Lys Thr Asp Ala
 20 25 30

gtc tgc ggt ttc cag gat cgg ata aga gcc ctg gtg gtg atc ccc atc 144
 Val Cys Gly Phe Gln Asp Arg Ile Arg Ala Leu Val Val Ile Pro Ile
 35 40 45

acg atg gtg gtc ctg ctt gct gtc ttg ttg gtg tct gcg tat atc aga 192
 Thr Met Val Val Leu Leu Ala Val Leu Leu Val Ser Ala Tyr Ile Arg
 50 55 60

aag gtg acc aag aag cca gag aat aag gtc ctc cag cct aag gct gtg 240
 Lys Val Thr Lys Lys Pro Glu Asn Lys Val Leu Gln Pro Lys Ala Val
 65 70 75 80

tcg cag gac cct gtg gag gac ttg gag gtc ctt cct gtc ccc ctc cac 288
 Ser Gln Asp Pro Val Glu Asp Leu Glu Val Leu Pro Val Pro Leu His
 85 90 95

ccc att gct ccg gtg cag gag acc tta cac ggg tgc cag ccg gtc acc 336
 Pro Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln Pro Val Thr
 100 105 110

<210> 61
 <211> 112
 <212> PRT
 <213> Felis catus

<400> 61
 Asn Val Ser Ser Ala Ser Glu Lys Cys His Pro Trp Thr Arg Cys Glu
 1 5 10 15
 Thr Lys Gly Leu Val Glu Leu Gln Ala Gly Thr Asn Lys Thr Asp Ala
 20 25 30
 Val Cys Gly Phe Gln Asp Arg Ile Arg Ala Leu Val Val Ile Pro Ile
 35 40 45
 Thr Met Val Val Leu Leu Ala Val Leu Leu Val Ser Ala Tyr Ile Arg
 50 55 60
 Lys Val Thr Lys Lys Pro Glu Asn Lys Val Leu Gln Pro Lys Ala Val
 65 70 75 80
 Ser Gln Asp Pro Val Glu Asp Leu Glu Val Leu Pro Val Pro Leu His
 85 90 95
 Pro Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln Pro Val Thr
 100 105 110

<210> 62
 <211> 336
 <212> DNA
 <213> Felis catus

<400> 62
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 aggaaggacc tccaagtcct ccacagggtc ctgcgacaca gccttaggct ggaggacctt 120
 attctctggc ttcttggtca cctttctgat atacgcagac accaacaaga cagcaagcag 180
 gaccaccatc gtgatgggga tcaccaccag ggctcttata cgatcctgga aaccgcagac 240
 ggcatccgtc ttgttggtcc ccgcctgaag ctccaccagg cctttggtct cacacctcgt 300
 ccaagggtga cacttttccg aagcagatga cacatt 336

<210> 63
 <211> 390
 <212> DNA
 <213> Canis familiaris

<400> 63
 ataagtgagg ctagtagtaa cccagcgtcc gttctgcggt gggcgccaaa aggggtactac 60
 accataagca gcaacctggt gagcctcgag aatgggaaac agttggccgt gaaaagacaa 120
 ggactctatt acgtctatgc ccaagtcacc ttctgctcca atcgggcagc ttcgagtcaa 180
 gctccgttcg tcgccagcct atgcctccat tccccgagtg gaacggagag agtcttactc 240
 cgcgccgcga gctcccgcgg ctgcgtccaaa ccttgccggcc aacagtccat ccacttgga 300
 ggagtatttg aattgcatcc aggtgcttcg gtgttcgtca acgtgactga tccaagccaa 360
 gtgagccacg ggaccggctt cacgtctttt 390

<210> 64
 <211> 1878
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (284)..(1063)

<400> 64
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 ttgctggga gagaagacta cgaagcacat ttccaggaa gtgtgggctg caacgattgt 180
 gcgctcttaa ctaatcctga gtaagggtggc cactttgaca gtgttttcat gctgcctctg 240
 ccaccttctc ggtctgaaga tatcatttca actctaacac agc atg atc gaa aca 295
 Met Ile Glu Thr
 1

tat agc caa act gct ccc cga tct gtg gcc act gga cca ccc gtc agt 343
 Tyr Ser Gln Thr Ala Pro Arg Ser Val Ala Thr Gly Pro Pro Val Ser
 5 10 15 20

atg aaa att ttt atg tat ttg ctt act gtt ttt ctc atc acc cag atg 391
 Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu Ile Thr Gln Met
 25 30 35

att gga tcg gca ctc ttt gct gta tat ctt cac aga aga ttg gac aag 439
 Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg Arg Leu Asp Lys
 40 45 50

ata gaa gat gaa agg aat ctt tat gaa gat ttt gtg ttc atg aaa acg 487
 Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe Met Lys Thr
 55 60 65

tta cag aaa tgc aac aaa ggg gag ggg tcc ttg tcc tta ctg aac tgt 535
 Leu Gln Lys Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu Leu Asn Cys
 70 75 80

gag gaa att aaa agc caa ttt gaa gcc ttt ctc aag gag ata atg cta 583
 Glu Glu Ile Lys Ser Gln Phe Glu Ala Phe Leu Lys Glu Ile Met Leu
 85 90 95 100

aac aac gaa atg aag aaa gaa gaa aac att gca atg caa aaa ggt gat 631
 Asn Asn Glu Met Lys Lys Glu Glu Asn Ile Ala Met Gln Lys Gly Asp
 105 110 115

cag gat cct cga att gca gcc cat gtc ata agt gag gct agt agt aac 679
 Gln Asp Pro Arg Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Asn
 120 125 130

cca gcg tcc gtt ctg cgg tgg gcg cca aaa ggg tac tac acc ata agc 727
 Pro Ala Ser Val Leu Arg Trp Ala Pro Lys Gly Tyr Tyr Thr Ile Ser
 135 140 145

agc aac ctg gtg agc ctc gag aat ggg aaa cag ttg gcc gtg aaa aga 775
 Ser Asn Leu Val Ser Leu Glu Asn Gly Lys Gln Leu Ala Val Lys Arg
 150 155 160

caa gga ctc tat tac gtc tat gcc caa gtc acc ttc tgc tcc aat cgg 823
 Gln Gly Leu Tyr Tyr Val Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg
 165 170 175 180

gca gct tcg agt caa gct ccg ttc gtc gcc agc cta tgc ctc cat tcc 871
 Ala Ala Ser Ser Gln Ala Pro Phe Val Ala Ser Leu Cys Leu His Ser
 185 190 195

ccg agt gga acg gag aga gtc tta ctc cgc gcc gcg agc tcc cgc ggc 919
 Pro Ser Gly Thr Glu Arg Val Leu Leu Arg Ala Ala Ser Ser Arg Gly
 200 205 210

tcg tcc aaa cct tgc ggc caa cag tcc atc cac ttg gga gga gta ttt 967
 Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe
 215 220 225

gaa ttg cat cca ggt gct tgc gtg ttc gtc aac gtg act gat cca agc 1015
 Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser
 230 235 240

caa gtg agc cac ggg acc ggc ttc acg tct ttt ggc tta ctc aaa ctc 1063
 Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu
 245 250 255 260

tgagtgtggtg cacctcacag gctgcagctc agctcctgtt ggtggtcttc gtaatacggc 1123
 cgagcagtta agaccaccac cctgttgaa ctgcctatatt ataaccctag gatcctcctc 1183
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 cttaacgtta aaaaaaaaaa aaaaaaaaaa aaaaa 1878

<210> 65

<211> 260

<212> PRT

<213> Canis familiaris

<400> 65

Met Ile Glu Thr Tyr Ser Gln Thr Ala Pro Arg Ser Val Ala Thr Gly

1	5	10	15
Pro Pro Val Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu	20	25	30
Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg	35	40	45
Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val	50	55	60
Phe Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ser Leu Ser	65	70	75
Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Ala Phe Leu Lys	85	90	95
Glu Ile Met Leu Asn Asn Glu Met Lys Lys Glu Glu Asn Ile Ala Met	100	105	110
Gln Lys Gly Asp Gln Asp Pro Arg Ile Ala Ala His Val Ile Ser Glu	115	120	125
Ala Ser Ser Asn Pro Ala Ser Val Leu Arg Trp Ala Pro Lys Gly Tyr	130	135	140
Tyr Thr Ile Ser Ser Asn Leu Val Ser Leu Glu Asn Gly Lys Gln Leu	145	150	155
Ala Val Lys Arg Gln Gly Leu Tyr Tyr Val Tyr Ala Gln Val Thr Phe	165	170	175
Cys Ser Asn Arg Ala Ala Ser Ser Gln Ala Pro Phe Val Ala Ser Leu	180	185	190
Cys Leu His Ser Pro Ser Gly Thr Glu Arg Val Leu Leu Arg Ala Ala	195	200	205
Ser Ser Arg Gly Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu	210	215	220
Gly Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val	225	230	235
Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly	245	250	255
Leu Leu Lys Leu			

<210> 66

<211> 1878

<212> DNA

<213> Canis familiaris

<400> 66

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tttcctttaa atacagtcac ttcaggagga ggagtgggca gcctctgctc tctcctccc 180
cctacactgg tggagaggca acaggggtga aataagataa ccgattagca acagcctgac 240
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gaaactggac taattatctg ccgtttactg aggattcaat ctgtgcataa tagtctcgtc 540
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tcttaccgac cggggcctgt tggcgctgcc cccgccctgt cattcccttc ttgcagccct 660
ccacgcctgg ggggtgataa taaatagtgc tccacgagga ggatcctagg gttataaata 720
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aggattagtt aagagcgcac aatcgttgca gccacactt cctggaaaat gtgcttcgta 1740
gtcttctctc ccagcaaaaa aagttacgta aagggttttt tttttttttt tttttttttt 1800
taattatacc catatcattc acttccaggc tttccctttt gttagtaaag aagaaacaag 1860
tttcttcttc catacatt 1878

<210> 67

<211> 780

<212> DNA

<213> Canis familiaris

<400> 67

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atgaaaattt ttatgtattt gcttactgtt tttctcatca ccagatgat tggatcggca 120
ctctttgctg tatactcttca cagaagattg gacaagatag aagatgaaag gaatctttat 180
gaagattttg tgttcatgaa aacgttacag aaatgcaaca aaggggaggg gtccttgtcc 240
ttactgaact gtgaggaaat taaaagccaa tttgaagcct ttctcaagga gataatgcta 300
aacaacgaaa tgaagaaaga agaaaacatt gcaatgcaaa aaggtgatca ggatcctcga 360
attgcagccc atgtcataag tgaggctagt agtaaccag cgtccgttct gcggtgggag 420
ccaaaagggt actacaccat aagcagcaac ctggtgagcc tcgagaatgg gaaacagttg 480

gccgtgaaaa gacaaggact ctattacgtc tatgcccaag tcaccttctg ctccaatcgg 540
gcagcttcga gtcaagctcc gttcgtcgcc agcctatgcc tccattcccc gagtggaacg 600
gagagagtct tactccgcgc cgcgagctcc cgcggctcgt ccaaaccttg cggccaacag 660
tccatccact tgggaggagt atttgaattg catccagggtg cttcgggtgtt cgtcaacgtg 720
actgatccaa gccaaagtgag ccacggggacc ggcttcacgt cttttggctt actcaaactc 780

<210> 68

<211> 780

<212> DNA

<213> Canis familiaris

<400> 68

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cacgttgacg aacaccgaag cacctggatg caattcaaact actcctccca agtggatgga 120
ctgttggccg caaggtttgg acgagccgcg ggagctcgcg gcgcggagta agactctctc 180
cgttccactc ggggaatgga ggcataggct ggcgacgaac ggagcttgac tcgaagctgc 240
ccgattggag cagaaggtga cttgggcata gacgtaatag agtccttgtc ttttcacggc 300
caactgtttc ccattctcga ggctcaccag gttgctgctt atgggtgtagt acccttttgg 360
cgcccaccgc agaacggacg ctgggttact actagcctca cttatgacat gggctgcaat 420
tcgaggatcc tgatcacctt tttgcattgc aatgttttct tctttcttca tttcgttggt 480
tagcattatc tccttgagaa aggcttcaaa ttggctttta atttctcac agttcagtaa 540
ggacaaggac ccctcccctt tgttgcatth ctgtaacgtt ttcatagaaca caaatcttc 600
ataaagattc ctttcatctt ctatcttgtc caatcttctg tgaagatata cagcaaagag 660
tgccgatcca atcatctggg tgatgagaaa aacagtaagc aaatacataa aaattttcat 720
actgacgggt ggtccagtgg ccacagatcg gggagcagtt tggctatatg tttcgatcat 780

<210> 69

<211> 633

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(633)

<400> 69

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 Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe
 1 5 10 15

atg aaa acg tta cag aaa tgc aac aaa ggg gag ggg tcc ttg tcc tta 96
 Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu
 20 25 30

ctg aac tgt gag gaa att aaa agc caa ttt gaa gcc ttt ctc aag gag 144
 Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Ala Phe Leu Lys Glu
 35 40 45

ata atg cta aac aac gaa atg aag aaa gaa gaa aac att gca atg caa 192
 Ile Met Leu Asn Asn Glu Met Lys Lys Glu Glu Asn Ile Ala Met Gln
 50 55 60

aaa ggt gat cag gat cct cga att gca gcc cat gtc ata agt gag gct 240
 Lys Gly Asp Gln Asp Pro Arg Ile Ala Ala His Val Ile Ser Glu Ala
 65 70 75 80

agt agt aac cca gcg tcc gtt ctg cgg tgg gcg cca aaa ggg tac tac 288
 Ser Ser Asn Pro Ala Ser Val Leu Arg Trp Ala Pro Lys Gly Tyr Tyr
 85 90 95

acc ata agc agc aac ctg gtg agc ctc gag aat ggg aaa cag ttg gcc 336
 Thr Ile Ser Ser Asn Leu Val Ser Leu Glu Asn Gly Lys Gln Leu Ala
 100 105 110

gtg aaa aga caa gga ctc tat tac gtc tat gcc caa gtc acc ttc tgc 384
 Val Lys Arg Gln Gly Leu Tyr Tyr Val Tyr Ala Gln Val Thr Phe Cys
 115 120 125

tcc aat cgg gca gct tcg agt caa gct ccg ttc gtc gcc agc cta tgc 432
 Ser Asn Arg Ala Ala Ser Ser Gln Ala Pro Phe Val Ala Ser Leu Cys
 130 135 140

ctc cat tcc ccg agt gga acg gag aga gtc tta ctc cgc gcc gcg agc 480
 Leu His Ser Pro Ser Gly Thr Glu Arg Val Leu Leu Arg Ala Ala Ser
 145 150 155 160

tcc cgc ggc tcg tcc aaa cct tgc ggc caa cag tcc atc cac ttg gga 528
 Ser Arg Gly Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly

	165	170	175	
gga gta ttt gaa ttg cat cca ggt gct tcg gtg ttc gtc aac gtg act				576
Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr				
	180	185	190	
gat cca agc caa gtg agc cac ggg acc ggc ttc acg tct ttt ggc tta				624
Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu				
	195	200	205	
ctc aaa ctc				633
Leu Lys Leu				
	210			
<210> 70				
<211> 211				
<212> PRT				
<213> Canis familiaris				
<400> 70				
Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe				
1 5 10 15				
Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu				
20 25 30				
Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Ala Phe Leu Lys Glu				
35 40 45				
Ile Met Leu Asn Asn Glu Met Lys Lys Glu Glu Asn Ile Ala Met Gln				
50 55 60				
Lys Gly Asp Gln Asp Pro Arg Ile Ala Ala His Val Ile Ser Glu Ala				
65 70 75 80				
Ser Ser Asn Pro Ala Ser Val Leu Arg Trp Ala Pro Lys Gly Tyr Tyr				
85 90 95				
Thr Ile Ser Ser Asn Leu Val Ser Leu Glu Asn Gly Lys Gln Leu Ala				
100 105 110				
Val Lys Arg Gln Gly Leu Tyr Tyr Val Tyr Ala Gln Val Thr Phe Cys				
115 120 125				
Ser Asn Arg Ala Ala Ser Ser Gln Ala Pro Phe Val Ala Ser Leu Cys				
130 135 140				

Leu His Ser Pro Ser Gly Thr Glu Arg Val Leu Leu Arg Ala Ala Ser
 145 150 155 160

Ser Arg Gly Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly
 165 170 175

Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr
 180 185 190

Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu
 195 200 205

Leu Lys Leu
 210

<210> 71

<211> 633

<212> DNA

<213> Canis familiaris

<400> 71

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 cacgttgacg aacaccgaag cacctggatg caattcaaact actcctccca agtggatgga 120
 ctgttgggccg caagggttgg acgagccgcg ggagctcgcg gcgcggagta agactctctc 180
 cgttccactc ggggaatgga ggcataaggct ggcgacgaac ggagcttgac tcgaagctgc 240
 ccgattggag cagaagggtga cttgggcata gacgtaatag agtccttgtc ttttcacggc 300
 caactgtttc ccattctcga ggctcaccag gttgctgctt atgggtgtagt acccttttgg 360
 cgcccaccgc agaacggacg ctgggttact actagcctca cttatgacat gggctgcaat 420
 tcgaggatcc tgatcacctt tttgcattgc aatgttttct tctttcttca tttcgttggt 480
 tagcattatc tccttgagaa aggcttcaaa ttggctttta atttcctcac agttcagtaa 540
 ggacaaggac ccctcccctt tgttgcattt ctgtaacggt ttcataaaca caaaatcttc 600
 ataaagattc ctttcatctt ctatcttgtc caa 633

<210> 72

<211> 885

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (29)..(808)

<400> 72

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gaagatacca tttcaacttt aacacagc atg atc gaa aca tat agc caa act      52
                        Met Ile Glu Thr Tyr Ser Gln Thr
                          1               5

gct ccc cgc tcc gtg gcc cct gga cca ccc gtc agt atg aaa att ttt      100
Ala Pro Arg Ser Val Ala Pro Gly Pro Pro Val Ser Met Lys Ile Phe
      10               15               20

atg tat tta ctt act gtg ttt ctc atc acc cag atg att ggg tca gca      148
Met Tyr Leu Leu Thr Val Phe Leu Ile Thr Gln Met Ile Gly Ser Ala
      25               30               35               40

ctc ttt gct gtg tat ctt cac aga aga ctg gac aag ata gaa gat gaa      196
Leu Phe Ala Val Tyr Leu His Arg Arg Leu Asp Lys Ile Glu Asp Glu
               45               50               55

agg aat ctt tat gaa gat ttt gtg ttc atg aaa aca tta cag aaa tgc      244
Arg Asn Leu Tyr Glu Asp Phe Val Phe Met Lys Thr Leu Gln Lys Cys
               60               65               70

aac aaa gga gag ggg gcc tta tcc tta ctg aac tgt gag gaa att aaa      292
Asn Lys Gly Glu Gly Ala Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys
               75               80               85

agc cgg ttt gaa gcc ttt ctc aag gag ata atg cta aac aaa gaa acg      340
Ser Arg Phe Glu Ala Phe Leu Lys Glu Ile Met Leu Asn Lys Glu Thr
               90               95               100

aag aaa gaa aaa aat gtt gca atg caa aaa ggc gac cag gat cct cga      388
Lys Lys Glu Lys Asn Val Ala Met Gln Lys Gly Asp Gln Asp Pro Arg
      105               110               115               120

gtt gca gca cat gtc ata agt gag gcc agc agt agc aca gcg tct gtt      436
Val Ala Ala His Val Ile Ser Glu Ala Ser Ser Ser Thr Ala Ser Val
               125               130               135

ctc cag tgg gcc ccc aaa ggc tac tac acc ata agc agc aac ttg gtg      484
Leu Gln Trp Ala Pro Lys Gly Tyr Tyr Thr Ile Ser Ser Asn Leu Val
               140               145               150

acc ctc gag aac ggg aag cag ctg gcc gtt aaa aga caa gga ctc tat      532

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Thr Leu Glu Asn Gly Lys Gln Leu Ala Val Lys Arg Gln Gly Leu Tyr
 155 160 165
 tat atc tac gcc caa gtc acc ttc tgt tcc aat cgg gaa gct tcg agt 580
 Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser
 170 175 180
 caa gct ccg ttc ata gcc agc ctc tgc ctg cat tcc ccg agt gga tcc 628
 Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu His Ser Pro Ser Gly Ser
 185 190 195 200
 gag aga gtc tta ctc aga gct gca aat gcc cgc agt tcc tcc aaa ccc 676
 Glu Arg Val Leu Leu Arg Ala Ala Asn Ala Arg Ser Ser Ser Lys Pro
 205 210 215
 tgt ggg cag caa tcc att cac ttg gga gga gtc ttc gaa ctg cat cca 724
 Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu His Pro
 220 225 230
 ggt gct tcg gtg ttc gtg aac gtg act gat ccg agc caa gtg agc cac 772
 Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His
 235 240 245
 ggg acg ggc ttc acg tct ttt ggc ttg ctc aaa ctc tgaacactgg 818
 Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu
 250 255 260
 cacctcgag gccgcgaggc ctgcaggccg cggctgagct cacgctggga gtcttcacaa 878
 tacagca 885

<210> 73

<211> 260

<212> PRT

<213> Felis catus

<400> 73

Met Ile Glu Thr Tyr Ser Gln Thr Ala Pro Arg Ser Val Ala Pro Gly
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Pro Pro Val Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
 20 25 30

Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg
 35 40 45

Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val

50

55

60

Phe Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ala Leu Ser
 65 70 75 80
 Leu Leu Asn Cys Glu Glu Ile Lys Ser Arg Phe Glu Ala Phe Leu Lys
 85 90 95
 Glu Ile Met Leu Asn Lys Glu Thr Lys Lys Glu Lys Asn Val Ala Met
 100 105 110
 Gln Lys Gly Asp Gln Asp Pro Arg Val Ala Ala His Val Ile Ser Glu
 115 120 125
 Ala Ser Ser Ser Thr Ala Ser Val Leu Gln Trp Ala Pro Lys Gly Tyr
 130 135 140
 Tyr Thr Ile Ser Ser Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu
 145 150 155 160
 Ala Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe
 165 170 175
 Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu
 180 185 190
 Cys Leu His Ser Pro Ser Gly Ser Glu Arg Val Leu Leu Arg Ala Ala
 195 200 205
 Asn Ala Arg Ser Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu
 210 215 220
 Gly Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val
 225 230 235 240
 Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly
 245 250 255
 Leu Leu Lys Leu
 260

<210> 74

<211> 885

<212> DNA

<213> Felis catus

<400> 74

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cctcccaagt gaatggattg ctgcccacag ggtttgagg aactgcgggc atttgcagct 240
ctgagtaaga ctctctcgga tccactcggg gaatgcaggc agaggctggc tatgaacgga 300
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ccttgtcttt taacggccag ctgcttccc ttctcgagg tcaccaagtt gctgcttatg 420
gtgtagtagc ctttgggggc ccactggaga acagacgctg tgctactgct ggcctcactt 480
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ttcttcgttt ctttgttttag cattatctcc ttgagaaagg cttcaaaccg gcttttaatt 600
tcctcacagt tcagtaagga taaggccccc tctcctttgt tgcatttctg taatgttttc 660
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agatacacag caaagagtgc tgaccaatc atctgggtga tgagaaacac agtaagtaaa 780
tacataaaaa ttttcatact gacgggtggt ccaggggcca cggagcggg agcagtttgg 840
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<210> 75

<211> 780

<212> DNA

<213> Felis catus

<400> 75

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gaagattttg tgttcatgaa aacattacag aaatgcaaca aaggagaggg ggccttatcc 240
ttactgaact gtgaggaaat taaaagccgg tttgaagcct ttctcaagga gataatgcta 300
aacaagaaa cgaagaaaga aaaaaatgtt gcaatgcaaa aaggcgacca ggatcctcga 360

gttgcagcac atgtcataag tgaggccagc agtagcacag cgtctgttct ccagtgggcc 420
cccaaaggct actacaccat aagcagcaac ttggtgaccc tcgagaacgg gaagcagctg 480
gccgttaaaa gacaaggact ctattatatac tacgcccaag tcaccttctg ttccaatcgg 540
gaagcttcga gtcaagctcc gttcatagcc agcctctgcc tgcattcccc gagtggatcc 600
gagagagtct tactcagagc tgcaaagcc cgcagttcct ccaaaccctg tgggcagcaa 660
tccattcact tgggaggagt cttcgaactg catccaggtg cttcgggtgtt cgtgaacgtg 720
actgatccga gccaaagtga ccacgggacg ggcttcacgt cttttggctt gctcaaactc 780

<210> 76

<211> 780

<212> DNA

<213> Felis catus

<400> 76

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ttgctgcca cagggtttgg aggaactgcg ggcatttgca gctctgagta agactctctc 180
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ccgattggaa cagaagggtga cttgggacga gatataatag agtccttgctc ttttaacggc 300
cagctgcttc ccgttctcga gggtcaccaa gttgctgctt atgggtgtagt agcctttggg 360
ggcccactgg agaacagacg ctgtgctact gctggcctca cttatgacat gtgctgcaac 420
tcgaggatcc tggtcgcctt tttgcattgc aacatttttt tctttcttcg tttctttggt 480
tagcattatc tccttgagaa aggcttcaaa ccggctttta atttcctcac agttcagtaa 540
ggataaggcc ccctctcctt tgttgcattt ctgtaatggt ttcattgaaca caaatcttc 600
ataaagattc ctttcattct ctatcttgct cagtcttctg tgaagataca cagcaaagag 660
tgctgacca atcatctggg tgatgagaaa cacagtaagt aaatacataa aaattttcat 720
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<210> 77

<211> 633

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(633)

<400> 77

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ctg gac aag ata gaa gat gaa agg aat ctt tat gaa gat ttt gtg ttc      48
Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe
   1             5             10             15

atg aaa aca tta cag aaa tgc aac aaa gga gag ggg gcc tta tcc tta      96
Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ala Leu Ser Leu
           20             25             30

ctg aac tgt gag gaa att aaa agc cgg ttt gaa gcc ttt ctc aag gag      144
Leu Asn Cys Glu Glu Ile Lys Ser Arg Phe Glu Ala Phe Leu Lys Glu
           35             40             45

ata atg cta aac aaa gaa acg aag aaa gaa aaa aat gtt gca atg caa      192
Ile Met Leu Asn Lys Glu Thr Lys Lys Glu Lys Asn Val Ala Met Gln
           50             55             60

aaa ggc gac cag gat cct cga gtt gca gca cat gtc ata agt gag gcc      240
Lys Gly Asp Gln Asp Pro Arg Val Ala Ala His Val Ile Ser Glu Ala
           65             70             75             80

agc agt agc aca gcg tct gtt ctc cag tgg gcc ccc aaa ggc tac tac      288
Ser Ser Ser Thr Ala Ser Val Leu Gln Trp Ala Pro Lys Gly Tyr Tyr
           85             90             95

acc ata agc agc aac ttg gtg acc ctc gag aac ggg aag cag ctg gcc      336
Thr Ile Ser Ser Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Ala
           100            105            110

gtt aaa aga caa gga ctc tat tat atc tac gcc caa gtc acc ttc tgt      384
Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys
           115            120            125

tcc aat cgg gaa gct tcg agt caa gct ccg ttc ata gcc agc ctc tgc      432
Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys
           130            135            140

ctg cat tcc ccg agt gga tcc gag aga gtc tta ctc aga gct gca aat      480

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Leu His Ser Pro Ser Gly Ser Glu Arg Val Leu Leu Arg Ala Ala Asn
 145 150 155 160
 gcc cgc agt tcc tcc aaa ccc tgt ggg cag caa tcc att cac ttg gga 528
 Ala Arg Ser Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly
 165 170 175
 gga gtc ttc gaa ctg cat cca ggt gct tcg gtg ttc gtg aac gtg act 576
 Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr
 180 185 190
 gat ccg agc caa gtg agc cac ggg acg ggc ttc acg tct ttt ggc ttg 624
 Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu
 195 200 205
 ctc aaa ctc 633
 Leu Lys Leu
 210

<210> 78
 <211> 211
 <212> PRT
 <213> Felis catus

<400> 78
 Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe
 1 5 10 15
 Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ala Leu Ser Leu
 20 25 30
 Leu Asn Cys Glu Glu Ile Lys Ser Arg Phe Glu Ala Phe Leu Lys Glu
 35 40 45
 Ile Met Leu Asn Lys Glu Thr Lys Lys Glu Lys Asn Val Ala Met Gln
 50 55 60
 Lys Gly Asp Gln Asp Pro Arg Val Ala Ala His Val Ile Ser Glu Ala
 65 70 75 80
 Ser Ser Ser Thr Ala Ser Val Leu Gln Trp Ala Pro Lys Gly Tyr Tyr
 85 90 95
 Thr Ile Ser Ser Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Ala
 100 105 110
 Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys

115	120	125
Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys		
130	135	140
Leu His Ser Pro Ser Gly Ser Glu Arg Val Leu Leu Arg Ala Ala Asn		
145	150	155
Ala Arg Ser Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly		
165	170	175
Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr		
180	185	190
Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu		
195	200	205
Leu Lys Leu		
210		

<210> 79

<211> 633

<212> DNA

<213> Felis catus

<400> 79

gagtttgagc aagccaaaag acgtgaagcc cgtcccgtgg ctcaactggc tcggatcagt 60
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 ttgctgcca cagggtttgg aggaactgcg ggcatttgca gctctgagta agactctctc 180
 ggatccactc ggggaatgca ggcagaggct ggctatgaac ggagcttgac tcgaagcttc 240
 ccgattggaa cagaaggtga cttgggcgta gatataatag agtccttgtc ttttaacggc 300
 cagctgcttc ccgttctcga gggtcaccaa gttgctgctt atgggtgtagt agcctttggg 360
 ggcccactgg agaacagacg ctgtgctact gctggcctca cttatgacat gtgctgcaac 420
 tcgaggatcc tggtcgcctt tttgcattgc aacatttttt tctttcttcg tttctttggt 480
 tagcattatc tccttgagaa aggcttcaaa ccggctttta atttcctcac agttcagtaa 540
 ggataaggcc ccctctcctt tgttgcattt ctgtaatggt ttcatgaaca caaatcttc 600
 ataaagattc ctttcatctt ctatcttgtc cag 633

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<220>  
<221> CDS  
<222> (29) .. (430)
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70

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 agaatgaggg ccaaccaaca gtagggactt aatggccagt ataactaagc ttcagagaca 550
 aagtaaatat ttcaggcatc ctactacttt atcacttcac acagatgaaa tatatttgag 610

<210> 81

<211> 134

<212> PRT

<213> Canis familiaris

<400> 81

Met Arg Met Leu Leu Asn Leu Ser Leu Leu Ala Leu Gly Ala Ala Tyr
 1 5 10 15

Val Ser Ala Phe Ala Val Glu Asn Pro Met Asn Arg Leu Val Ala Glu
 20 25 30

Thr Leu Thr Leu Leu Ser Thr His Arg Thr Trp Leu Ile Gly Asp Gly
 35 40 45

Asn Leu Met Ile Pro Thr Pro Glu Asn Lys Asn His Gln Leu Cys Ile
 50 55 60

Lys Glu Val Phe Gln Gly Ile Asp Thr Leu Lys Asn Gln Thr Ala His
 65 70 75 80

Gly Glu Ala Val Asp Lys Leu Phe Gln Asn Leu Ser Leu Ile Lys Glu
 85 90 95

His Ile Glu Arg Gln Lys Lys Arg Cys Ala Gly Glu Arg Trp Arg Val
 100 105 110

Thr Lys Phe Leu Asp Tyr Leu Gln Val Phe Leu Gly Val Ile Asn Thr
 115 120 125

Glu Trp Thr Pro Glu Ser
 130

<210> 82

<211> 610

<212> DNA

<213> Canis familiaris

<400> 82

ctcaaata tttcatctgt gtgaagtgat aaagtagtag gatgcctgaa atatttactt 60

tgtctctgaa gcttagttat actggccatt aagtcctac tggtggttg ccctcattct 120
catcgccaaa aaaccattct tctccaaaat cttccactac aataagccgg ttgttctca 180
actttccggg gtccactcgg tgtttattac accaagaaat acttgcagg agtctaggaa 240
ctttgtcact ctccatcttt ctctgcaca cttttttttt tggcgctcta tgtgttcttt 300
tattaaagac aagttttgga atagtttata cacagcctcc ccgtgggcag ttgggttctt 360
caatgtgtct ataccctgaa aaacttcttt aatgcacagt tggtgatttt tattttcagg 420
agtaggaatc atcaggttcc catcgctat cagccaagtt cgatgagtgg agagcagtgt 480
caaggctctt gccaccagtc tattcatggg attttctaca gcaaaggcag aaacataggc 540
agccccaaga gctagcaaac tcaaattcag aagcattctc atagctctga aatgttcagt 600
gtttgccttg 610

<210> 83
<211> 402
<212> DNA
<213> Canis familiaris

<400> 83
atgagaatgc ttctgaattt gagtttgcta gctcttgggg ctgcctatgt ttctgccttt 60
gctgtagaaa atcccatgaa tagactgggt gcagagacct tgacactgct ctccactcat 120
cgaacttggc tgataggcga tgggaacctg atgattccta ctctgaaaa taaaaatcac 180
caactgtgca ttaaagaagt ttttcagggt atagacacat tgaagaacca aactgcccac 240
ggggaggctg tggataaact attccaaaac ttgtctttaa taaaagaaca catagagcgc 300
caaaaaaaaaa ggtgtgcagg agaaagatgg agagtgacaa agttcctaga ctacctgcaa 360
gtatttcttg gtgtaataaa caccgagtgg acaccggaaa gt 402

<210> 84
<211> 402
<212> DNA
<213> Canis familiaris

<400> 84

actttccggt gtccactcgg tgtttattac accaagaaat acttgcaggt agtctaggaa 60
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 tattaagac aagttttgga atagtttata cacagcctcc ccgtgggcag tttgggtctt 180
 caatgtgtct ataccctgaa aaacttcttt aatgcacagt tgggtatttt tattttcagg 240
 agtaggaatc atcaggttcc catcgctat cagccaagtt cgatgagtgg agagcagtgt 300
 caaggtctct gccaccagtc tattcatggg attttctaca gcaaaggcag aaacataggc 360
 agccccaaga gctagcaaac tcaaattcag aagcattctc at 402

<210> 85

<211> 345

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(345)

<400> 85

ttt gct gta gaa aat ccc atg aat aga ctg gtg gca gag acc ttg aca 48
 Phe Ala Val Glu Asn Pro Met Asn Arg Leu Val Ala Glu Thr Leu Thr
 1 5 10 15

ctg ctc tcc act cat cga act tgg ctg ata ggc gat ggg aac ctg atg 96
 Leu Leu Ser Thr His Arg Thr Trp Leu Ile Gly Asp Gly Asn Leu Met
 20 25 30

att cct act cct gaa aat aaa aat cac caa ctg tgc att aaa gaa gtt 144
 Ile Pro Thr Pro Glu Asn Lys Asn His Gln Leu Cys Ile Lys Glu Val
 35 40 45

ttt cag ggt ata gac aca ttg aag aac caa act gcc cac ggg gag gct 192
 Phe Gln Gly Ile Asp Thr Leu Lys Asn Gln Thr Ala His Gly Glu Ala
 50 55 60

gtg gat aaa cta ttc caa aac ttg tct tta ata aaa gaa cac ata gag 240
 Val Asp Lys Leu Phe Gln Asn Leu Ser Leu Ile Lys Glu His Ile Glu
 65 70 75 80

cgc caa aaa aaa agg tgt gca gga gaa aga tgg aga gtg aca aag ttc 288
 Arg Gln Lys Lys Arg Cys Ala Gly Glu Arg Trp Arg Val Thr Lys Phe

85

90

95

cta gac tac ctg caa gta ttt ctt ggt gta ata aac acc gag tgg aca 336
 Leu Asp Tyr Leu Gln Val Phe Leu Gly Val Ile Asn Thr Glu Trp Thr
 100 105 110

ccg gaa agt
 Pro Glu Ser
 115

345

<210> 86
 <211> 115
 <212> PRT
 <213> Canis familiaris

<400> 86
 Phe Ala Val Glu Asn Pro Met Asn Arg Leu Val Ala Glu Thr Leu Thr
 1 5 10 15

Leu Leu Ser Thr His Arg Thr Trp Leu Ile Gly Asp Gly Asn Leu Met
 20 25 30

Ile Pro Thr Pro Glu Asn Lys Asn His Gln Leu Cys Ile Lys Glu Val
 35 40 45

Phe Gln Gly Ile Asp Thr Leu Lys Asn Gln Thr Ala His Gly Glu Ala
 50 55 60

Val Asp Lys Leu Phe Gln Asn Leu Ser Leu Ile Lys Glu His Ile Glu
 65 70 75 80

Arg Gln Lys Lys Arg Cys Ala Gly Glu Arg Trp Arg Val Thr Lys Phe
 85 90 95

Leu Asp Tyr Leu Gln Val Phe Leu Gly Val Ile Asn Thr Glu Trp Thr
 100 105 110

Pro Glu Ser
 115

<210> 87
 <211> 345
 <212> DNA
 <213> Canis familiaris

<400> 87

actttccggt gtccactcgg tgtttattac accaagaaat acttgcaggt agtctaggaa 60
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tattaaagac aagttttgga atagtttatc cacagcctcc ccgtgggcag ttgggttctt 180
caatgtgtct ataccctgaa aaacttcttt aatgcacagt tggtgatttt tattttcagg 240
agtaggaatc atcaggttcc catcgcttat cagccaagtt cgatgagtgg agagcagtgt 300
caaggtctct gccaccagtc tattcatggg attttctaca gcaaa 345

<210> 88

<211> 166

<212> DNA

<213> Canis familiaris

<400> 88

ctcagcttag gccagcctac gacctgctg ctcttccctc gctcctcctg cattggctct 60
gggctccatg ggcgtctggt tgactgtggt cattgctctc acctgcctcg gtggccttgc 120
ctccccgagc cctgtgactc cctccccaac cctcaaggag ctcat 166

<210> 89

<211> 272

<212> DNA

<213> Canis familiaris

<400> 89

tggccttgcc tccccgagcc ctgtgactcc ctccccaacc ctcaaggagc tcattgagga 60
gctgggtcaac atcaccaga atcaggcatc cctctgcaac ggcagcatgg tgtggagcgt 120
caacctgacc gccggcatgt actgcgcagc tctagaatct ctgatcaatg tctccgactg 180
cagcgccatc caaaggaccc agaggatgct gaaagcactg tgctctcaaa agcccgcggc 240
agggcagatt tccagtgaac gcagccgaga ca 272

<210> 90

<211> 278

<212> DNA

<213> Canis familiaris

<400> 90

atggcgctct ggttgactgt ggtcattgct ctcacctgcc tcggtggcct tgcctccccg 60
 agccctgtga ctccctcccc aaccctcaag gagctcattg aggagctggt caacatcacc 120
 cagaatcagg catccctctg caacggcagc atggtgtgga gcgtcaacct gaccgccggc 180
 atgtactgcg cagctctaga atctctgatc aatgtctccg actgcagcgc catccaaagg 240
 acccagagga tgctgaaagc actgtgctct caaaagcc 278

<210> 91

<211> 1302

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (52)..(444)

<400> 91

ctacgacctg cctgctcttc cctcgctcct cctgcattgg ctctgggctc c atg gcg 57
 Met Ala
 1

ctc tgg ttg act gtg gtc att gct ctc acc tgc ctc ggt ggc ctt gcc 105
 Leu Trp Leu Thr Val Val Ile Ala Leu Thr Cys Leu Gly Gly Leu Ala
 5 10 15

tcc ccg agc cct gtg act ccc tcc cca acc ctc aag gag ctc att gag 153
 Ser Pro Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu
 20 25 30

gag ctg gtc aac atc acc cag aat cag gca tcc ctc tgc aac ggc agc 201
 Glu Leu Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser
 35 40 45 50

atg gtg tgg agc gtc aac ctg acc gcc ggc atg tac tgc gca gct cta 249
 Met Val Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu
 55 60 65

gaa tct ctg atc aat gtc tcc gac tgc agc gcc atc caa agg acc cag 297
 Glu Ser Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln
 70 75 80

agg atg ctg aaa gca ctg tgc tct caa aag ccc gcg gca ggg cag att 345
 Arg Met Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Gln Ile

85

90

95

tcc agt gaa cgc agc cga gac acc aaa att gaa gtg atc cag ttg gtg 393
Ser Ser Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val
100 105 110

aaa aac ctg ctc acc tat gta agg gga gtt tat cgc cat gga aat ttc 441
Lys Asn Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe
115 120 125 130

aga tgaagcatga aaacttagca tccttatctg tagaccacaga cctgaccact 494
Arg

taagttccag attcattttt ctttccgacg tcacaaattt cttagggagg tggggggggg 554
ggagaaccat ttcctcagct gggacctcag cctgcaccgc ctgcctccat ggagctgagc 614
ccagccaccc ctgccttggt gcatggggcc cagccgggtg gccctcctcc gtctgcactt 674
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gcattacagt ggaggcagat atgtgtggga gggggtcttg ctgtacctgg gagtggcaca 794
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gccaagcagt aatttattgt ttttccttgt atttaaagtt aagaaataaa atatgttatc 1094
aaagagttaa taatatatag aagagtagcc taaaaggctg catttggtgt gtgtggccag 1154
gccggggcgg gtggggggga ggggtgtgtc actgaatgtg ctctttcact gactttgtca 1214
aactggaagc cagaaataaa gatggtgaca agagaaaaaa aaaaaaaaaa aaaaaaaaaa 1274
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1302

<210> 92

<211> 131

<212> PRT

<213> Canis familiaris

<400> 92

Met Ala Leu Trp Leu Thr Val Val Ile Ala Leu Thr Cys Leu Gly Gly
 1 5 10 15
 Leu Ala Ser Pro Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu
 20 25 30
 Ile Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn
 35 40 45
 Gly Ser Met Val Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala
 50 55 60
 Ala Leu Glu Ser Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg
 65 70 75 80
 Thr Gln Arg Met Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly
 85 90 95
 Gln Ile Ser Ser Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln
 100 105 110
 Leu Val Lys Asn Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly
 115 120 125
 Asn Phe Arg
 130

<210> 93

<211> 1302

<212> DNA

<213> Canis familiaris

<400> 93

tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt ttttctcttg 60
 tcaccatctt tatttctggc ttccagtttg acaaagtcag tgaaagagca cattcagtga 120
 caacaccctc cccccaccc gccccggcct ggccacacac accaaatgca gccttttagg 180
 ctactcttct atatattatt aactctttga taacatattt tatttcttaa ctttaaatac 240
 aaggaaaaac aataaattac tgcttggttg agggccagct gctgagtggc agacaagagc 300
 agcatctctg accctttctc ctgtcccctg tgtcggcccc aggatcccag tgaggtagca 360
 gaattttaca cacagtgttt attcccaggg actctctaaa cccgagtcac tgggccccca 420

gctccaagcc actccctgtc cccagcacia acaaagacac ttgtttaaat aacacacaat 480
aataaataag gctaagaaga aacatgtctg tgccactccc aggtacagca agaccccctc 540
ccacacatat ctgcctccac tgtaatgctg cactttgctc tgaggagggg acagtcattg 600
gatgcagtgc tttccctcag cgttgatgaa gtgcagacgg aggagggcca cccggctggg 660
ccccatgcac caaggcaggg gtggctgggc tcagctccat ggaggcaggc ggtgcaggct 720
gaggtcccag ctgaggaaat ggttctcccc cccccacc tccctaagaa atttgtgacg 780
tcggaaagaa aatgaatct ggaacttaag tggtcaggct tgggtctaca gataaggatg 840
ctaagttttc atgcttcac tcgaaatttc atggcgataa actcccctta catagggtgag 900
caggtttttc accaactgga tcacttcaat tttggtgtct cggctgcgtt cactggaaat 960
ctgccctgcc gggggtttt gagagcacag tgctttcagc atcctctggg tcctttggat 1020
ggcgctgcag tcggagacat tgatcagaga ttctagagct gcgcagtaca tgccggcggt 1080
caggttgacg ctccacacca tgctgccgtt gcagagggat gctgattct gggatgatt 1140
gaccagctcc tcaatgagct ccttgagggt tggggaggga gtcacagggc tcggggaggc 1200
aaggccaccg aggcaggatg gagcaatgac cacagtcaac cagagcgcca tggagcccag 1260
agccaatgca ggaggagcga gggaagagca ggcaggctct ag 1302

<210> 94

<211> 393

<212> DNA

<213> Canis familiaris

<400> 94

atggcgctct ggttgactgt ggtcattgct ctacctgcc tcggtggcct tgccctcccg 60
agccctgtga ctccctccc aacctcaag gagctcattg aggagctggt caacatcacc 120
cagaatcagg catccctctg caacggcagc atggtgtgga gcgtcaacct gaccgccggc 180
atgtactgcg cagctctaga atctctgac aatgtctccg actgcagcgc catccaaagg 240
accagagga tgctgaaagc actgtgctct caaaagcccg cggcagggca gatttccagt 300
gaacgcagcc gagacaccaa aattgaagt atccagttgg tgaaaaacct gctcacctat 360

gtaaggggag tttatcgcca tggaaatttc aga

393

<210> 95

<211> 393

<212> DNA

<213> Canis familiaris

<400> 95

tctgaaattt ccatggcgat aaactcccct tacataggtg agcaggtttt tcaccaactg 60
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ttgagagcac agtgctttca gcatcctctg ggtcctttgg atggcgctgc agtcggagac 180
attgatcaga gattctagag ctgcgcagta catgccggcg gtcagggtga cgctccacac 240
catgctgccg ttgcagaggg atgcctgatt ctgggtgatg ttgaccagct cctcaatgag 300
ctccttgagg gttggggagg gagtcacagg gctcggggag gcaaggccac cgaggcaggt 360
gagagcaatg accacagtca accagagcgc cat 393

<210> 96

<211> 333

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(333)

<400> 96

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1 5 10 15
gtc aac atc acc cag aat cag gca tcc ctc tgc aac ggc agc atg gtg 96
Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser Met Val
20 25 30
tgg agc gtc aac ctg acc gcc ggc atg tac tgc gca gct cta gaa tct 144
Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser
35 40 45
ctg atc aat gtc tcc gac tgc agc gcc atc caa agg acc cag agg atg 192

Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln Arg Met
 50 55 60

ctg aaa gca ctg tgc tct caa aag ccc gcg gca ggg cag att tcc agt 240
 Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Gln Ile Ser Ser
 65 70 75 80

gaa cgc agc cga gac acc aaa att gaa gtg atc cag ttg gtg aaa aac 288
 Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val Lys Asn
 85 90 95

ctg ctc acc tat gta agg gga gtt tat cgc cat gga aat ttc aga 333
 Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe Arg
 100 105 110

<210> 97

<211> 111

<212> PRT

<213> Canis familiaris

<400> 97

Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu Glu Leu
 1 5 10 15

Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser Met Val
 20 25 30

Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser
 35 40 45

Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln Arg Met
 50 55 60

Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Gln Ile Ser Ser
 65 70 75 80

Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val Lys Asn
 85 90 95

Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe Arg
 100 105 110

<210> 98

<211> 333

<212> DNA

<213> Canis familiaris

<400> 98

tctgaaattt ccatggcgat aaactcccct tacataggtg agcaggtttt tcaccaactg 60
 gatcacttca attttggtgt ctgggtgcg ttcaactggaa atctgccttg ccgcgggctt 120
 ttgagagcac agtgctttca gcatcctctg ggtcctttgg atggcgctgc agtcggagac 180
 attgatcaga gattctagag ctgcgcagta catgccggcg gtcaggttga cgctccacac 240
 catgctgccg ttgcagaggg atgcctgatt ctgggtgatg ttgaccagct cctcaatgag 300
 ctcccttgagg gttggggagg gagtcacagg gct 333

<210> 99

<211> 1269

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (57)..(446)

<400> 99

ccagcctacg acctgcctgc tcttccctcg ctccctcctgc attggctctg ggctcc atg 59
 Met
 1

gcg ctc tgg ttg act gtg gtc att gct ctc acc tgc ctc ggt ggc ctt 107
 Ala Leu Trp Leu Thr Val Val Ile Ala Leu Thr Cys Leu Gly Gly Leu
 5 10 15

gcc tcc ccg agc cct gtg act ccc tcc cca acc ctc aag gag ctc att 155
 Ala Ser Pro Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile
 20 25 30

gag gag ctg gtc aac atc acc cag aat cag gca tcc ctc tgc aac ggc 203
 Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly
 35 40 45

agc atg gtg tgg agc gtc aac ctg acc gcc ggc atg tac tgc gca gct 251
 Ser Met Val Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
 50 55 60 65

cta gaa tct ctg atc aat gtc tcc gac tgc agc gcc atc caa agg acc 299
 Leu Glu Ser Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr
 70 75 80

cag agg atg ctg aaa gca ctg tgc tct caa aag ccc gcg gca ggg att 347
 Gln Arg Met Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Ile
 85 90 95

tcc agt gaa cgc agc cga gac acc aaa att gaa gtg atc cag ttg gtg 395
 Ser Ser Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val
 100 105 110

aaa aac ctg ctc acc tat gta agg gga gtt tat cgc cat gga aat ttc 443
 Lys Asn Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe
 115 120 125

aga tgaagcatga aaacttagca tccttatctg tagaccaga cctgaccact 496
 Arg
 130

taagttccag attcattttt ctttccgacg tcacaaattt cttagggagg tggggggggg 556
 ggagaaccat ttcctcagct gggacctcag cctgcaccgc ctgcctccat ggagctgagc 616
 ccagccaccc ctgccttggt gcatggggcc cagccgggtg gccctcctcc gtctgcactt 676
 catcaacgct gagggaaagc actgcatccc atgactgtcc cctcctcaga gcaaagtgca 736
 gcattacagt ggaggcagat atgtgtggga ggggtcttg ctgtacctgg gagtggcaca 796
 gacatgtttc ttcttagcct tatttattat tgtgtgttat ttaaacaagt gtctttgttt 856
 gtgctgggga cagggagtgg cttggagctg ggggccagct gactcgggtt tagagagtcc 916
 ctgggaataa gcactgtgtg taaaattctg ctacctact gggatcctgg ggccgacaca 976
 ggggacagga gaaagggtca gagatgctgc tcttgtctgc cactcagcag ctggccctca 1036
 gccaaagcagt aatttattgt ttttccttgt atttaaagtt aagaaataaa atatgttacc 1096
 aaagagttaa taatatatag aagagtagcc taaaaggctg catttggtgt gtgtggccag 1156
 gccggggcgg gtggggggga ggggtgtgtc actgaatgtg ctctttcact gactttgtca 1216
 aactggaagc cagaaataaa gatggtgaca agagaaaaaa aaaaaaaaaa aaa 1269

<210> 100

<211> 130

<212> PRT

<213> Canis familiaris

<400> 100

Met Ala Leu Trp Leu Thr Val Val Ile Ala Leu Thr Cys Leu Gly Gly
 1 5 10 15

Leu Ala Ser Pro Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu
 20 25 30

Ile Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn
 35 40 45

Gly Ser Met Val Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala
 50 55 60

Ala Leu Glu Ser Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg
 65 70 75 80

Thr Gln Arg Met Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly
 85 90 95

Ile Ser Ser Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu
 100 105 110

Val Lys Asn Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn
 115 120 125

Phe Arg
 130

<210> 101

<211> 1269

<212> DNA

<213> Canis familiaris

<400> 101

tttttttttt tttttttttt tcttgtcacc atctttatatt ctggcttcca gtttgacaaa 60
 gtcagtga aa gagcacattc agtgacaaca cctccccccc caccgcccc ggcctggcca 120
 cacacaccaa atgcagcctt ttaggctact cttctatata ttattaactc tttgataaca 180
 tattttatatt cttaacttta aatacaagga aaaacaataa attactgctt ggctgagggc 240
 cagctgctga gtggcagaca agagcagcat ctctgaccct ttctcctgtc cctgtgtcgc 300
 gccccaggat cccagtgagg tagcagaatt ttacacacag tgcttattcc cagggactct 360

ctaaaccoga gtcactgggc cccagctcc aagccactcc ctgtccccag cacaaacaaa 420
gacacttggt taaataacac acaataataa ataaggctaa gaagaaacat gtctgtgcca 480
ctcccaggta cagcaagacc cctcccaca catatctgcc tccactgtaa tgctgcactt 540
tgctctgagg aggggacagt catgggatgc agtgctttcc ctcagcgttg atgaagtgca 600
gacggaggag ggccacccgg ctgggccccca tgcaccaagg caggggtggc tgggctcagc 660
tccatggagg caggcgggtgc aggctgaggt cccagctgag gaaatgggtc tcccccccc 720
ccacctccct aagaaatttg tgacgtcggg aagaaaaatg aatctggaac ttaagtggtc 780
aggtctgggt ctacagataa ggatgctaag ttttcatgct tcatctgaaa tttccatggc 840
gataaactcc ccttacatag gtgagcaggt ttttcaccaa ctggatcact tcaatttttg 900
tgtctcggct gcgttccactg gaaatccctg ccgcgggctt ttgagagcac agtgctttca 960
gcacctctg ggtccttttg atggcgctgc agtcggagac attgatcaga gattctagag 1020
ctgcgcagta catgccggcg gtcaggttga cgctccacac catgctgccg ttgcagaggg 1080
atgcctgatt ctgggtgatg ttgaccagct cctcaatgag ctcttgagg gttggggagg 1140
gagtcacagg gctcggggag gcaaggccac cgaggcaggt gagagcaatg accacagtca 1200
accagagcgc catggagccc agagccaatg caggaggagc gagggaagag caggcaggtc 1260
gtaggctgg 1269

<210> 102

<211> 390

<212> DNA

<213> Canis familiaris

<400> 102

atggcgctct ggttgactgt ggtcattgct ctcacctgcc tcggtggcct tgcctccccg 60
agccctgtga ctccctcccc aacctcaag gagctcattg aggagctggg caacatcacc 120
cagaatcagg catccctctg caacggcagc atggtgtgga gcgtcaacct gaccgccggc 180
atgtactgcg cagctctaga atctctgatc aatgtctccg actgcagcgc catccaaagg 240
accagagga tgctgaaagc actgtgctct caaaagcccc cggcagggat ttccagtga 300

cgcagccgag acaccaaaat tgaagtgatc cagttggtga aaaacctgct cacctatgta 360
 aggggagttt atcgccatgg aaatttcaga 390

<210> 103
 <211> 390
 <212> DNA
 <213> Canis familiaris

<400> 103
 tctgaaattt ccatggcgat aaactcccct tacataggtg agcaggtttt tcaccaactg 60
 gatcacttca attttggtgt ctgggtgctg ttacttgga atccctgccg cgggcttttg 120
 agagcacagt gctttcagca tcctctgggt cctttggatg gcgctgcagt cggagacatt 180
 gatcagagat tctagagctg cgcagtacat gccggcggtc aggttgacgc tccacaccat 240
 gctgccgttg cagaggggatg cctgattctg ggtgatgttg accagctcct caatgagctc 300
 cttgagggtt ggggagggag tcacagggtc cggggaggca aggccaccga ggcagggtgag 360
 agcaatgacc acagtcaacc agagcgccat 390

<210> 104
 <211> 330
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (1)..(330)

<400> 104
 agc cct gtg act ccc tcc cca acc ctc aag gag ctc att gag gag ctg 48
 Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu Glu Leu
 1 5 10 15
 gtc aac atc acc cag aat cag gca tcc ctc tgc aac ggc agc atg gtg 96
 Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser Met Val
 20 25 30
 tgg agc gtc aac ctg acc gcc ggc atg tac tgc gca gct cta gaa tct 144
 Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser
 35 40 45

ctg atc aat gtc tcc gac tgc agc gcc atc caa agg acc cag agg atg 192
 Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln Arg Met
 50 55 60

ctg aaa gca ctg tgc tct caa aag ccc gcg gca ggg att tcc agt gaa 240
 Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Ile Ser Ser Glu
 65 70 75 80

cgc agc cga gac acc aaa att gaa gtg atc cag ttg gtg aaa aac ctg 288
 Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val Lys Asn Leu
 85 90 95

ctc acc tat gta agg gga gtt tat cgc cat gga aat ttc aga 330
 Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe Arg
 100 105 110

<210> 105

<211> 110

<212> PRT

<213> Canis familiaris

<400> 105

Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu Glu Leu
 1 5 10 15

Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser Met Val
 20 25 30

Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser
 35 40 45

Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln Arg Met
 50 55 60

Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Ile Ser Ser Glu
 65 70 75 80

Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val Lys Asn Leu
 85 90 95

Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe Arg
 100 105 110

<210> 106

<211> 330

<212> DNA

<213> Canis familiaris

<400> 106

tctgaaattt ccatggcgat aaactcccct tacataggtg agcaggtttt tcaccaactg 60
gatcacttca attttggtgt ctcggtgcg ttcactggaa atccctgccg cgggcttttg 120
agagcacagt gctttcagca tcctctgggt cctttggatg gcgctgcagt cggagacatt 180
gatcagagat tctagagctg cgcagtacat gccggcggtc aggttgacgc tccacaccat 240
gctgccgttg cagagggatg cctgattctg ggtgatgttg accagctcct caatgagctc 300
cttgagggtt ggggagggag tcacagggt 330

<210> 107

<211> 567

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(567)

<400> 107

atg gcg ctg ccc tct tcc ttc ttg gtg gcc ctg gtg gcg ctg ggc tgc 48
Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
1 5 10 15
aac tcc gtc tgc tct ctg ggc tgt gac ctg cct cag acc cac ggc ctg 96
Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
20 25 30
ctg aac agg agg gcc ttg acg ctc ctg gga caa atg agg aga ctc cct 144
Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
35 40 45
gcc agc tcc tgt cag aag gac aga aat gac ttc gcc ttc ccc cag gac 192
Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp
50 55 60
gtg ttt ggt gga gac cag tcc cac aag gcc caa gcc ctc tcg gtg gtg 240
Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
65 70 75 80
cac gtg acg aac cag aag atc ttc cac ttc ttc tgc aca gag gcg tcc 288

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser
 85 90 95
 tcg tct gct gct tgg aac acc acc ctc ctg gag gaa ttc tgc acg gga 336
 Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
 100 105 110
 ctt gat tgg cag ctg acc cgc ctg gaa gcc tgt gtc atg cag gag gtg 384
 Leu Asp Trp Gln Leu Thr Arg Leu Glu Ala Cys Val Met Gln Glu Val
 115 120 125
 ggg gag gga gag gct ccc ctc acg aac gag gac tcc atc ctg agg aac 432
 Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Ile Leu Arg Asn
 130 135 140
 tac ttc caa aga ctc tcc ctc tac ctg caa gag aag aaa tac agc cct 480
 Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro
 145 150 155 160
 tgt gcc tgg gag atc gtc aga gca gaa atc atg aga tcc ttg tat tat 528
 Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr
 165 170 175
 tca tca aca gcc ttg cag aaa aga tta agg agc gag aaa 567
 Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
 180 185
 <210> 108
 <211> 189
 <212> PRT
 <213> Felis catus
 <400> 108
 Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
 1 5 10 15
 Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
 20 25 30
 Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
 35 40 45
 Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp
 50 55 60
 Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
 65 70 75 80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser
 85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
 100 105 110

Leu Asp Trp Gln Leu Thr Arg Leu Glu Ala Cys Val Met Gln Glu Val
 115 120 125

Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Ile Leu Arg Asn
 130 135 140

Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro
 145 150 155 160

Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr
 165 170 175

Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
 180 185

<210> 109
 <211> 567
 <212> DNA
 <213> Felis catus

<400> 109
 tttctcgctc cttaatcttt tctgcaaggc tgttgatgaa taatacaagg atctcatgat 60
 ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120
 gagtctttgg aagtagttcc tcaggatgga gtccctcggtc gtgaggggag cctctccctc 180
 cccacacctc tgcacgacac aggcttccag gcgggtcagc tgccaatcaa gtcccgtgca 240
 gaattcctcc aggagggtgg tgttccaagc agcagacgag gacgcctctg tgcagaagaa 300
 gtggaagatc ttctgggtcg tcacgtgcac caccgagagg gcttgggcct tgtgggactg 360
 gtctccacca aacacgtcct gggggaaggc gaagtcattt ctgtccttct gacaggagct 420
 ggcagggagt ctctcattt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480
 ggtctgaggc aggtcacagc ccagagagca gacggagttg cagcccagcg ccaccagggc 540
 caccaagaag gaagagggca gcgccat 567

<210> 110

<211> 567

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(567)

<400> 110

atg gcg ctg ccc tct tcc ttc ttg gtg gcc ctg gtg gcg ctg ggc tgc 48
 Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
 1 5 10 15

aac tcc gtc tgc tct ctg ggc tgt gac ctg cct cag acc cac ggc ctg 96
 Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
 20 25 30

ctg aac agg agg gcc ttg acg ctc ctg gga caa atg agg aga ctc cct 144
 Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
 35 40 45

gcc agc tcc tgt cag aag gac agg aat gac ttc gcc ttc ccc cag gac 192
 Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp
 50 55 60

gtg ttc ggt gga gac cag tcc cac aag gct caa gcc ctc tcg gtg gtg 240
 Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
 65 70 75 80

cac gtg acg aac cag gag atc ttc cac ttc ttc tgc aca gag gcg tcc 288
 His Val Thr Asn Gln Glu Ile Phe His Phe Phe Cys Thr Glu Ala Ser
 85 90 95

tcg tct gct gct tgg aac acc acc ctc ctg gag gaa ttc tgc acg gga 336
 Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
 100 105 110

ctt gat cgg cag ctg acc cgc ctg gaa gcc tgt gtc gtg cag gag gtg 384
 Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Val Gln Glu Val
 115 120 125

ggg gag gga gag gct ccc ctc acg aac gag gac tcc ctc ctg agg aac 432
 Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Leu Leu Arg Asn
 130 135 140

tac ttc caa aga ctc tcc ctc tac ctg caa gag aag aaa tac agc cct 480
 Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro
 145 150 155 160

tgt gcc tgg gag atc gtc aga gca gaa atc atg aga tcc ttg tat tat 528
 Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr
 165 170 175

tca tca aca gcc ttg caa aaa aga tta agg agc gag aaa 567
 Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
 180 185

<210> 111
 <211> 189
 <212> PRT
 <213> Felis catus

<400> 111
 Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
 1 5 10 15

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
 20 25 30

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
 35 40 45

Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp
 50 55 60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
 65 70 75 80

His Val Thr Asn Gln Glu Ile Phe His Phe Phe Cys Thr Glu Ala Ser
 85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
 100 105 110

Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Val Gln Glu Val
 115 120 125

Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Leu Leu Arg Asn
 130 135 140

Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro
 145 150 155 160

Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr
 165 170 175

Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
 180 185

<210> 112

<211> 567

<212> DNA

<213> Felis catus

<400> 112

tttctcgctc cttaatcttt ttgcaaggc tgttgatgaa taatacaagg atctcatgat 60
 ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120
 gagtctttgg aagtagttcc tcaggaggga gtccctcggtc gtgaggggag cctctccctc 180
 cccacacctc tgcacgacac aggcttccag gcgggtcagc tgccgatcaa gtcccgtgca 240
 gaattcctcc aggaggggtgg tgttccaagc agcagacgag gacgcctctg tgcagaagaa 300
 gtggaagatc tcttggttcg tcacgtgcac caccgagagg gcttgagcct tgtgggactg 360
 gtctccaccg aacacgtcct gggggaaggc gaagtcattc ctgtccttct gacaggagct 420
 ggcagggagt ctctcatatt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480
 ggtctgaggc aggtcacagc ccagagagca gacggagttg cagcccagcg ccaccagggc 540
 caccaagaag gaagagggca gcgccat 567

<210> 113

<211> 498

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(498)

<400> 113

tgt gac ctg cct cag acc cac ggc ctg ctg aac agg agg gcc ttg acg 48
 Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
 1 5 10 15

ctc ctg gga caa atg agg aga ctc cct gcc agc tcc tgt cag aag gac 96
 Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp
 20 25 30

aga aat gac ttc gcc ttc ccc cag gac gtg ttt ggt gga gac cag tcc 144
 Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
 35 40 45

cac aag gcc caa gcc ctc tcg gtg gtg cac gtg acg aac cag aag atc 192
 His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile
 50 55 60

ttc cac ttc ttc tgc aca gag gcg tcc tcg tct gct gct tgg aac acc 240
 Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr
 65 70 75 80

acc ctc ctg gag gaa ttc tgc acg gga ctt gat tgg cag ctg acc cgc 288
 Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Trp Gln Leu Thr Arg
 85 90 95

ctg gaa gcc tgt gtc atg cag gag gtg ggg gag gga gag gct ccc ctc 336
 Leu Glu Ala Cys Val Met Gln Glu Val Gly Glu Gly Glu Ala Pro Leu
 100 105 110

acg aac gag gac tcc atc ctg agg aac tac ttc caa aga ctc tcc ctc 384
 Thr Asn Glu Asp Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu
 115 120 125

tac ctg caa gag aag aaa tac agc cct tgt gcc tgg gag atc gtc aga 432
 Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg
 130 135 140

gca gaa atc atg aga tcc ttg tat tat tca tca aca gcc ttg cag aaa 480
 Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys
 145 150 155 160

aga tta agg agc gag aaa 498
 Arg Leu Arg Ser Glu Lys
 165

<210> 114

<211> 166

<212> PRT

<213> Felis catus

<400> 114

Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
 1 5 10 15

Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp
 20 25 30

Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
 35 40 45

His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile
 50 55 60

Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr
 65 70 75 80

Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Trp Gln Leu Thr Arg
 85 90 95

Leu Glu Ala Cys Val Met Gln Glu Val Gly Glu Gly Glu Ala Pro Leu
 100 105 110

Thr Asn Glu Asp Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu
 115 120 125

Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg
 130 135 140

Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys
 145 150 155 160

Arg Leu Arg Ser Glu Lys
 165

<210> 115

<211> 498

<212> DNA

<213> Felis catus

<400> 115

tttctcgctc cttaatcttt tctgcaaggc tggtgatgaa taatacaagg atctcatgat 60

ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120

gagtctttgg aagtagttcc tcaggatgga gtcctcggtc gtgaggggag cctctccctc 180

ccccacctcc tgcattgacac aggcattccag gcgggtcagc tgccaatcaa gtcccgtgca 240

gaattcctcc aggaggggtgg tgttccaagc agcagacgag gacgcctctg tgcagaagaa 300
 gtggaagatc ttctgggttcg tcacgtgcac caccgagagg gcttgggcct tgtgggactg 360
 gtctccacca aacacgtcct gggggaaggc gaagtcattt ctgtccttct gacaggagct 420
 ggcaggaggt ctcctcattt gtcccaggag cgtcaaggcc ctcctgttca gcaggccgtg 480
 ggtctgaggc aggtcaca 498

<210> 116

<211> 498

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(498)

<400> 116

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Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr	
1 5 10 15	
ctc ctg gga caa atg agg aga ctc cct gcc agc tcc tgt cag aag gac	96
Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp	
20 25 30	
agg aat gac ttc gcc ttc ccc cag gac gtg ttc ggt gga gac cag tcc	144
Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser	
35 40 45	
cac aag gct caa gcc ctc tcg gtg gtg cac gtg acg aac cag gag atc	192
His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Glu Ile	
50 55 60	
ttc cac ttc ttc tgc aca gag gcg tcc tcg tct gct gct tgg aac acc	240
Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr	
65 70 75 80	
acc ctc ctg gag gaa ttc tgc acg gga ctt gat cgg cag ctg acc cgc	288
Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg	
85 90 95	
ctg gaa gcc tgt gtc gtg cag gag gtg ggg gag gga gag gct ccc ctc	336
Leu Glu Ala Cys Val Val Gln Glu Val Gly Glu Gly Glu Ala Pro Leu	
100 105 110	

acg aac gag gac tcc ctc ctg agg aac tac ttc caa aga ctc tcc ctc 384
 Thr Asn Glu Asp Ser Leu Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu
 115 120 125

tac ctg caa gag aag aaa tac agc cct tgt gcc tgg gag atc gtc aga 432
 Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg
 130 135 140

gca gaa atc atg aga tcc ttg tat tat tca tca aca gcc ttg caa aaa 480
 Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys
 145 150 155 160

aga tta agg agc gag aaa 498
 Arg Leu Arg Ser Glu Lys
 165

<210> 117
 <211> 166
 <212> PRT
 <213> Felis catus

<400> 117
 Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
 1 5 10 15

Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp
 20 25 30

Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
 35 40 45

His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Glu Ile
 50 55 60

Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr
 65 70 75 80

Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg
 85 90 95

Leu Glu Ala Cys Val Val Gln Glu Val Gly Glu Gly Glu Ala Pro Leu
 100 105 110

Thr Asn Glu Asp Ser Leu Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu
 115 120 125

Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg
 130 135 140

Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys
 145 150 155 160

Arg Leu Arg Ser Glu Lys
 165

<210> 118
 <211> 498
 <212> DNA
 <213> Felis catus

<400> 118
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 ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120
 gagtctttgg aagtagttcc tcaggaggga gtcctcgttc gtgaggggag cctctccctc 180
 cccacctcc tgcacgacac aggcttccag gcgggtcagc tgccgatcaa gtcccgtgca 240
 gaattcctcc aggagggtgg tgttccaagc agcagacgag gacgcctctg tgcagaagaa 300
 gtggaagatc tcttggttcg tcacgtgcac caccgagagg gcttgagcct tgtgggactg 360
 gtctccaccg aacacgtcct gggggaaggc gaagtcattc ctgtccttct gacaggagct 420
 ggcagggagt ctctcathtt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480
 ggtctgaggc aggtcaca 498

<210> 119
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 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (10)..(441)

<400> 119
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 Met Trp Leu Gln Asn Leu Leu Phe Leu Gly Thr Val Val Cys
 1 5 10

agc atc tct gca ccc acc agt tca ccc agc tct gtc act cgg ccc tgg 99
 Ser Ile Ser Ala Pro Thr Ser Ser Pro Ser Ser Val Thr Arg Pro Trp
 15 20 25 30

 caa cac gtg gat gcc atc aag gag gcc ctg agc ctt ctg aac aac agt 147
 Gln His Val Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asn Ser
 35 40 45

 agt gaa ata act gct gtg atg aat gaa gca gta gaa gtc gtc tct gaa 195
 Ser Glu Ile Thr Ala Val Met Asn Glu Ala Val Glu Val Val Ser Glu
 50 55 60

 atg ttt gac cct gag gag ccg aaa tgc ctg cag act cac cta aag ctg 243
 Met Phe Asp Pro Glu Glu Pro Lys Cys Leu Gln Thr His Leu Lys Leu
 65 70 75

 tac gag cag ggc cta cgg ggc agc ctc atc agc ctc aag gag cct ctg 291
 Tyr Glu Gln Gly Leu Arg Gly Ser Leu Ile Ser Leu Lys Glu Pro Leu
 80 85 90

 aga atg atg gcc aac cat tac aag cag cac tgc ccc ctt act ccg gaa 339
 Arg Met Met Ala Asn His Tyr Lys Gln His Cys Pro Leu Thr Pro Glu
 95 100 105 110

 acg ccc tgt gaa acc cag act atc acc ttc aaa aat ttc aaa gag aat 387
 Thr Pro Cys Glu Thr Gln Thr Ile Thr Phe Lys Asn Phe Lys Glu Asn
 115 120 125

 ctg aag gat ttt ctg ttt aac aac ccc ttt gac tgc tgg gga cca gac 435
 Leu Lys Asp Phe Leu Phe Asn Asn Pro Phe Asp Cys Trp Gly Pro Asp
 130 135 140

 cag aag taa 444
 Gln Lys

<210> 120

<211> 144

<212> PRT

<213> Felis catus

<400> 120

Met Trp Leu Gln Asn Leu Leu Phe Leu Gly Thr Val Val Cys Ser Ile
 1 5 10 15

Ser Ala Pro Thr Ser Ser Pro Ser Ser Val Thr Arg Pro Trp Gln His
 20 25 30

Val Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asn Ser Ser Glu
 35 40 45

Ile Thr Ala Val Met Asn Glu Ala Val Glu Val Val Ser Glu Met Phe
 50 55 60

Asp Pro Glu Glu Pro Lys Cys Leu Gln Thr His Leu Lys Leu Tyr Glu
 65 70 75 80

Gln Gly Leu Arg Gly Ser Leu Ile Ser Leu Lys Glu Pro Leu Arg Met
 85 90 95

Met Ala Asn His Tyr Lys Gln His Cys Pro Leu Thr Pro Glu Thr Pro
 100 105 110

Cys Glu Thr Gln Thr Ile Thr Phe Lys Asn Phe Lys Glu Asn Leu Lys
 115 120 125

Asp Phe Leu Phe Asn Asn Pro Phe Asp Cys Trp Gly Pro Asp Gln Lys
 130 135 140

<210> 121

<211> 444

<212> DNA

<213> Felis catus

<400> 121

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 ctctttgaaa tttttgaagg tgatagtctg ggtttcacag ggcgtttccg gagtaagggg 120
 gcagtgctgc ttgtaatggt tggccatcat tctcagaggc tccttgaggc tgatgaggct 180
 gccccgtagg ccctgctcgt acagcttttag gtgagtctgc aggcatttcg gctcctcagg 240
 gtcaaacatt tcagagacga cttctactgc ttcattcatc acagcagtta tttcactact 300
 gttgttcaga aggctcaggg cctccttgat ggcattccacg tggtgccagg gccgagtgac 360
 agagctgggt gaactggtgg gtgcagagat gctgcagacc acagtgccca ggaaaagcag 420
 gttctgcagc cacatggtgg atcc 444

<210> 122

<211> 432

<212> DNA

<213> Felis catus

<400> 122

atgtggctgc agaacctgct tttcctgggc actgtggtct gcagcatctc tgcacccacc 60
agttcaccca gctctgtcac tcggccctgg caacacgtgg atgccatcaa ggaggccctg 120
agccttctga acaacagtag tgaaataact gctgtgatga atgaagcagt agaagtcgtc 180
tctgaaatgt ttgaccctga ggagccgaaa tgctgcaga ctcacctaaa gctgtacgag 240
cagggcctac ggggcagcct catcagcctc aaggagcctc tgagaatgat ggccaaccat 300
tacaagcagc actgccccct tactccggaa acgccctgtg aaaccagac tatcaccttc 360
aaaaatttca aagagaatct gaaggatttt ctgtttaaca acccctttga ctgctgggga 420
ccagaccaga ag 432

<210> 123

<211> 432

<212> DNA

<213> Felis catus

<400> 123

cttctggtct ggtccccagc agtcaaaggg gttgttaaac agaaaatcct tcagattctc 60
tttgaaattt ttgaaggtga tagtctgggt ttcacagggc gtttccggag taagggggca 120
gtgctgcttg taatggttgg ccatcattct cagaggctcc ttgaggctga tgaggctgcc 180
ccgtaggccc tgctcgtaca gctttaggtg agtctgcagg catttcggct cctcagggtc 240
aaacatttca gagacgactt ctactgcttc attcatcaca gcagttattt cactactggt 300
gttcagaagg ctcagggcct ccttgatggc atccacgtgt tgccagggcc gagtgacaga 360
gctgggtgaa ctggtgggtg cagagatgct gcagaccaca gtgcccagga aaagcaggtt 420
ctgcagccac at 432

<210> 124

<211> 381

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(381)

<400> 124

gca ccc acc agt tca ccc agc tct gtc act cgg ccc tgg caa cac gtg 48
 Ala Pro Thr Ser Ser Pro Ser Ser Val Thr Arg Pro Trp Gln His Val
 1 5 10 15

gat gcc atc aag gag gcc ctg agc ctt ctg aac aac agt agt gaa ata 96
 Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asn Ser Ser Glu Ile
 20 25 30

act gct gtg atg aat gaa gca gta gaa gtc gtc tct gaa atg ttt gac 144
 Thr Ala Val Met Asn Glu Ala Val Glu Val Val Ser Glu Met Phe Asp
 35 40 45

cct gag gag ccg aaa tgc ctg cag act cac cta aag ctg tac gag cag 192
 Pro Glu Glu Pro Lys Cys Leu Gln Thr His Leu Lys Leu Tyr Glu Gln
 50 55 60

ggc cta cgg ggc agc ctc atc agc ctc aag gag cct ctg aga atg atg 240
 Gly Leu Arg Gly Ser Leu Ile Ser Leu Lys Glu Pro Leu Arg Met Met
 65 70 75 80

gcc aac cat tac aag cag cac tgc ccc ctt act ccg gaa acg ccc tgt 288
 Ala Asn His Tyr Lys Gln His Cys Pro Leu Thr Pro Glu Thr Pro Cys
 85 90 95

gaa acc cag act atc acc ttc aaa aat ttc aaa gag aat ctg aag gat 336
 Glu Thr Gln Thr Ile Thr Phe Lys Asn Phe Lys Glu Asn Leu Lys Asp
 100 105 110

ttt ctg ttt aac aac ccc ttt gac tgc tgg gga cca gac cag aag 381
 Phe Leu Phe Asn Asn Pro Phe Asp Cys Trp Gly Pro Asp Gln Lys
 115 120 125

<210> 125

<211> 127

<212> PRT

<213> Felis catus

<400> 125

Ala Pro Thr Ser Ser Pro Ser Ser Val Thr Arg Pro Trp Gln His Val
 1 5 10 15

Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asn Ser Ser Glu Ile
 20 25 30
 Thr Ala Val Met Asn Glu Ala Val Glu Val Val Ser Glu Met Phe Asp
 35 40 45
 Pro Glu Glu Pro Lys Cys Leu Gln Thr His Leu Lys Leu Tyr Glu Gln
 50 55 60
 Gly Leu Arg Gly Ser Leu Ile Ser Leu Lys Glu Pro Leu Arg Met Met
 65 70 75 80
 Ala Asn His Tyr Lys Gln His Cys Pro Leu Thr Pro Glu Thr Pro Cys
 85 90 95
 Glu Thr Gln Thr Ile Thr Phe Lys Asn Phe Lys Glu Asn Leu Lys Asp
 100 105 110
 Phe Leu Phe Asn Asn Pro Phe Asp Cys Trp Gly Pro Asp Gln Lys
 115 120 125

<210> 126
 <211> 381
 <212> DNA
 <213> Felis catus

<400> 126
 cttctgggtct ggtccccagc agtcaaaggg gttgttaaac agaaaatcct tcagattctc 60
 tttgaaatttt ttgaaggtga tagtctgggt ttcacagggc gtttccggag taagggggca 120
 gtgctgcttg taatggttgg ccatcattct cagaggctcc ttgaggctga tgaggctgcc 180
 ccgtaggccc tgctcgta ca gctttaggtg agtctgcagg catttcggct cctcagggtc 240
 aaacatttca gagacgactt ctactgcttc attcatcaca gcagttattt cactactgtt 300
 gttcagaagg ctcagggcct ccttgatggc atccacgtgt tgccagggcc gagtgacaga 360
 gctgggtgaa ctggtgggtg c 381

<210> 127
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 <212> DNA
 <213> Artificial Sequence

<400> 127

cctcgagatt cagctttcaa tgcctgta

28

<210> 128

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 128

tgcccrstcg gcttcttctc c

21

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 129

cgactctctt trccrtctctc ctg

23

<210> 130

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 130

cctcaaattg cggcacatgt c

21

<210> 131

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 131

ctgttcagag ttgagtaag cc

22

<210> 132

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 132

gaagatacca tttcaacttt aacacagc

28

<210> 133

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 133

tgctgtattg tgaagactcc cagc

24

<210> 134

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 134

atgcactttc tttgcc

16

<210> 135

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 135

ctggaggaaa akacttcrat gattctgata tctgaaatat at

42

<210> 136

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 136

ctgacycttk sttggscctc attctca

27

<210> 137

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 137

gggctcgaga aaagatttgc tgtagaaaat cccatg

36

<210> 138

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 138

cccgcggccg ctcaactttc cggtgtccac tc

32

<210> 139

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 139

gtcmtggctc tyrcttgcct tgg

23

<210> 140

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 140

aaastgggcy acytcgattt tgg

23

<210> 141

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 141

gtgatgttg yagctcctc

20

<210> 142

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 142

aattaaccct cactaaaggg

20

<210> 143

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 143

atggcgctct gggtgactgt

20

<210> 144

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 144

ggcttttgag agcacagtgc

20

<210> 145

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 145

ccccatatga gccctgtgac tccctcccc

29

<210> 146

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Primer

<400> 146

ggggaattct catctgaaat ttccatggcg

30

<210> 147

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 147

atggcgctgc cctcttcctt ctg

24

<210> 148

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 148

tcatttctcg ctccttaatc ttttctgc

28

<210> 149

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 149

caggatcca ccatgtggct gcagaacctg cttttcc

37

<210> 150

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 150

ttactttctgg tctgggtcccc agcagtcaaa ggggttggtta aacagaaaat

50

<210> 151

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 151

cacagyccca tctcctcc

18

<210> 152

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 152

gtaatacgac tcactatagg gc

22

<210> 153

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

Primer

<400> 153

acggaattcg agatgatagt gctggc

26

<210> 154

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 154

gtgtctagat ttggtagaaa aggatgat

28

SEQUENCE LISTING

<110> Sim, Sek-Kee
 Yang, Shumin
 Dreitz, Matthew J.
 Wonderling, Ramani S.

<120> CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
 ACID MOLECULES, AND USES THEREOF

<130> IM-2-C1-PCT

<140> not yet assigned

<141> 1999-05-28

<150> 60/087,306

<151> 1998-05-29

<160> 154

<170> PatentIn Ver. 2.0

<210> 1

<211> 549

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (43)..(438)

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tcc caa ctg att cca act ctg gtc tgc tta cta gca ctc acc agc acc 102
 Ser Gln Leu Ile Pro Thr Leu Val Cys Leu Leu Ala Leu Thr Ser Thr
 5 10 15 20

ttt gtc cac gga cat aac ttc aat att act att aaa gag atc atc aaa 150
 Phe Val His Gly His Asn Phe Asn Ile Thr Ile Lys Glu Ile Ile Lys
 25 30 35

atg ttg aac atc ctc acc ggc aga aac gac tgc tgc atg gag ctg act 190
 Met Leu Asn Ile Leu Thr Ala Arg Asn Asp Ser Cys Met Glu Leu Thr
 40 45 50

gtc aag gac gtc ttc act gct cca aag aac aca agc gct aag gaa atc 246
 Val Lys Asp Val Phe Thr Ala Pro Lys Asn Thr Ser Asp Lys Glu Ile
 55 60 65

ttc tgc aga gct gct act gta ctg cgg cag atc tat aca cac aac tgc 290
 Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Ile Tyr Thr His Asn Cys
 70 75 80

tcc aac aga tat ctc aga gga ctc tac agg aac ctc agc agt atg gca 342
 Ser Asn Arg Tyr Leu Arg Gly Leu Tyr Arg Asn Leu Ser Ser Met Ala
 85 90 95 100

aac aag acc tgt tct atg aat gaa atc aag aag agt aca ctg aac gac 390
 Asn Lys Thr Cys Ser Met Asn Glu Ile Lys Lys Ser Thr Leu Lys Asp
 105 110 115

ttc ttg gaa agg cta aaa gtg atc atg cag aag aaa tac tac agg cat. 438
 Phe Leu Glu Arg Leu Lys Val Ile Met Gln Lys Lys Tyr Tyr Arg His
 120 125 130

tgaagctgaa tcttttaatt tatgagtttt taaatagctt tattttaaaa atatttatat 490

atttataaca taataaataa aatatatat agaaaaaaa aaaaaaaa a 549

<210> 2

<211> 132

<212> PRT

<213> Canis familiaris

<400> 2

Met Gly Leu Thr Ser Gln Leu Ile Pro Thr Leu Val Cys Leu Leu Ala
 1 5 10 15

Leu Thr Ser Thr Phe Val His Gly His Asn Phe Asn Ile Thr Ile Lys
 20 25 30

Glu Ile Ile Lys Met Leu Asn Ile Leu Thr Ala Arg Asn Asp Ser Cys
 35 40 45

Met Glu Leu Thr Val Lys Asp Val Phe Thr Ala Pro Lys Asn Thr Ser
 50 55 60

Asp Lys Glu Ile Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Ile Tyr
 65 70 75 80

Thr His Asn Cys Ser Asn Arg Tyr Leu Arg Gly Leu Tyr Arg Asn Leu
 85 90 95

Ser Ser Met Ala Asn Lys Thr Cys Ser Met Asn Glu Ile Lys Lys Ser
 100 105 110

Thr Leu Lys Asp Phe Leu Glu Arg Leu Lys Val Ile Met Gln Lys Lys
 115 120 125

Tyr Tyr Arg His
 130

<210> 3

<211> 549

<212> DNA

<213> Canis familiaris

<400> 3

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 gtattttctt tgcctgatca cttttagcct ttccaaagag tctttcagtg tactcttctt 180
 gatttcattc atagaaacag tcttgtttgc catgctgctg aggttcctgt agagtccctt 240
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 gaagatttcc ttatcgtctg tcttcttttg agcagtgag agtcccttga cagtcagctc 360
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 aatattgaag ttatgtccgt ggcacaaggt gctgggtgag gctagtasgc agaccagagt 480
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 cctcgtgcc 549

<210> 4

<211> 395

<212> DNA

<213> Canis familiaris

<400> 4

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ctcacagcga gaaacgactc gtgcatggag ctgactgtca aggacgtctt cactgtctcc 180
 aagacaccaa gcgataagga aatcttctgc agagctgcta ctgtactgcg gcagatctat 240
 acacacaact gctccaacag atatctcaga ggactctaca ggaacctcag cagcatggca 300
 aacaagacct gtcttatgaa tgaatcaag aagagtacac tgaagacctt ctgggaagg 360
 ctaaaagtga tcctgcagaa gaaatactac aggcac 396

<210> 5

<211> 396

<212> DNA

<213> Canis familiaris

<400> 5

atgcctgtag tattcttctt gcctgatcac ttttagcctt tccaagcagt ctctcagctg 60
 actcttcttg atttcattca tagaacaggc ctgtgttgcg atgctgctga ggttctctga 120
 gagtctcttg agatatctgt tggagcagtt gtgtgtatag atctgcgcga gtacagttag 180
 agctctgcag aagcttctct tctcctctgt gttctttgga gcagtgaaga cgtctctgac 240
 agtcagctcc atgcacgagt cgtttctcgc tctgaggatg ttcaacattt tgatgatctc 300
 tttcaatagta atattgaagt tatgtccgtg gacaaaggcg ctggtgagtg ctagtacgca 360
 gaccagagtt ggaatcagtt gggaggtgag acccat 396

<210> 6

<211> 1013

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> [35]..(916)

<400> 6

atctgaccat aggcctgagc ggcctccggc cagc atg ata gtc ctg gcg cca gcc 55
 Met Ile Val Leu Ala Pro Ala
 1 5

tgg agc cca act gcc tcc ctg ttg ctg ctg ctg ctg ctg agc ccc ggc 103
 Trp Ser Pro Thr Ala Ser Leu Leu Leu Leu Leu Leu Ser Pro Gly

10	15	20	
ctc cgc ggg acc ecc gac tgc tcc ttc agc cac agc ecc atc tcc tcc			151
Leu Arg Gly Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser			
25	30	35	
acc ttc ggc gtc acc atc cgc aag ctg tct gat tac ctg ctt cag gac			199
Thr Phe Ala Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp			
40	45	50	55
tat cca gtc act gtc gcc tcc aac ctg cag gac gac gag ctc tgc ggg			247
Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly			
60	65	70	
ggc ttc tgg cgc ctg gtc ctg gcc cag cgc tgg atg gtg cgg ctc cag			295
Ala Phe Trp Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln			
75	80	85	
gct gtg gct gga tcc caa atg caa atc ctg ctg gag gct gtc aac acc			343
Ala Val Ala Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr			
90	95	100	
gag ata cac ttt gtc acc ttc tgt gcc ttc cag ecc ctc ecc agc tgt			391
Glu Ile His Phe Val Thr Phe Cys Ala Phe Gln Pro Leu Pro Ser Cys			
105	110	115	
ctt cgc ttc gtc cag acc aac atc tcc cac ctc ctg cag gac acc tcc			439
Leu Arg Phe Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser			
120	125	130	135
cag cag ctg gcc gcc ctg aag ccc tgg atc acc cgc agg aat ttc tcc			487
Gln Gln Leu Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser			
140	145	150	
ggg tgc ctg gag ctg cag tgt cag ecc gac tcc tct aca ttg gtg ccc			535
Gly Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro			
155	160	165	
cca agg agc ccc ggg gcc ctg gag gcc act gcc ttg cca gcc cct cag			583
Pro Arg Ser Pro Gly Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln			
170	175	180	
gca cct cgg ctg ctc ctc ctg ctg ctg ctg ccc gtg gct ctc ctg ctg			631
Ala Pro Arg Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu			
185	190	195	
atg tcc act gcc tgg tgc ctg cat tgg cga agg agg cgg cgg cgg agg			679
Met Ser Thr Ala Trp Cys Leu His Trp Arg Arg Arg Arg Arg Arg Arg			

200	205	210	215	
tca ccc tac cct ggg gag cag agg aca ctg agg ccc agc gag cgg agc				727
Ser Pro Tyr Pro Gly Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser				
	220	225	230	
cat ctg ccc gag gac aca gag ctg gga cct gga ggg agt cag cta ggg				775
His Leu Pro Glu Asp Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu				
	235	240	245	
act ggt ccc ttc ctc gac cac gca gcc ccg ctc gct ccc tcc cca gga				823
Thr Gly Pro Phe Leu Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly				
	250	255	260	
tca agg caa cgc ccg ccc cca acg ccc cca aag cca gcc cca gcc cca				871
Ser Arg Gln Arg Pro Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro				
	265	270	275	
cct ctc ccc ctc tgt aca aag tcc ttg ccc cca aga aat tgt ata				916
Pro Leu Pro Leu Cys Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile				
	280	285	290	
taaatcattc tttttaccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa				976
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa				1013
<210> 7				
<211> 294				
<212> PRT				
<213> Canis familiaris				
<400> 7				
Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Ala Ser Leu Leu Leu				
1 5 10 15				
Leu Leu Leu Leu Ser Pro Gly Leu Arg Gly Thr Pro Asp Cys Ser Phe				
20 25 30				
Ser His Ser Pro Ile Ser Ser Thr Phe Ala Val Thr Ile Arg Lys Leu				
35 40 45				
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu				
50 55 60				
Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp Arg Leu Val Leu Ala Gln				
65 70 75 80				

Arg Trp Met Val Arg Leu Gln Ala Val Ala Gly Ser Gln Met Gln Ile
 85 90 95

 Leu Leu Glu Ala Val Asn Thr Glu Ile His Phe Val Thr Phe Cys Ala
 100 105 110

 Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 115 120 125

 His Leu Leu Gln Asp Thr Ser Gln Gln Leu Ala Ala Leu Lys Pro Trp
 130 135 140

 Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu Gln Cys Gln Pro
 145 150 155 160

 Asp Ser Ser Thr Leu Val Pro Pro Arg Ser Pro Gly Ala Leu Glu Ala
 165 170 175

 Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu Leu Leu Leu Leu
 180 185 190

 Leu Pro Val Ala Leu Leu Leu Met Ser Thr Ala Trp Cys Leu His Trp
 195 200 205

 Arg Arg Arg Arg Arg Arg Arg Ser Pro Tyr Pro Gly Glu Gln Arg Thr
 210 215 220

 Leu Arg Pro Ser Glu Arg Ser His Leu Pro Glu Asp Thr Glu Leu Gly
 225 230 235 240

 Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu Asp His Ala Ala
 245 250 255

 Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro Pro Pro Thr Pro
 260 265 270

 Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro Leu Cys Thr Lys Ser Leu
 275 280 285

 Pro Pro Arg Asn Cys Ile
 290

<210> 8

<211> 1013

<212> DNA

<213> Canis familiaris

<400> 8

tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60
 tttttttttt tttttttttt tagaaaagga tgatttatat acaattttttt ggggggcaagg 120
 actttgtaca gagggggaga ggtggggctg gggctggctt tgggggctgt gggggcgggc 180
 gttgccttga tctgggggag ggagcgagcg gggctggctg gtcgagggaag ggaccagtct 240
 ctgctgact cctccaggt cccagctctg tgtctctggg cagatggctc cgctcgctgg 300
 gctcagtggt cctctgctcc ccagggtagg gtgacctccg ccgacgctc ctccgccaat 360
 gcaggcacca ggcagtggaac atcagcagga gaggccaggg cagcagcagc aggaggagca 420
 gccgaggtgc ctgagggggt ggcaaggcag tggcctccag ggcgccgggg ctccctgggg 480
 gcaccaatgt agaggagtcg ggctgacact gcagctccag gcacccggag aaattcctgc 540
 gggatgacca gggcttcagg ggggcagct gctgggaggt gtctgcagg aggtgggaga 600
 tgttggctctg gacgaagcga agacagctgg ggaggggctg gaaggcacag aaggtgacaa 660
 agtgtatctc cgtgttgaca gctccagca ggatttgcct ttgggatcca gccacagcct 720
 ggagccgcaac catccagcgc tgggcagga ccaggcgcca gaacgcccc cagagctcgt 780
 cgtctgcag gttggaggcg acagtgaact gatagtctg agcaggtaa tcgacagct 840
 tgcggatggt gaccgcgag gtggaggaga tggggctgtg gctgaaggag cagtcggggg 900
 tcccgaggag gccggggctg agcagcagca gcagcaacag ggaggcagtt gggctccagg 960
 ctggcgccag cactatcact tcggccggag gccctcctg cctatggta gat 1013

<210> 9

<211> 882

<212> DNA

<213> Canis familiaris

<400> 9

atgatagtgc tggcgccagc ctggagccca actgcctccc tgttgcctgt gctgctgctc 60
 agccccggcc tccgggggac ccccgactgc tcttcagcc acagccccat ctctccccc 120
 ttccgggtca cctccgca gctgtctgat tccctgcttc aggaatatcc agtcactgtc 180

gcctccaacc tgcaggacga cgagctctgc ggggcgttct ggcgcctggc cctggccacg 240
 cgctggatgg tgcggctcca ggcctgtggt ggatccnasa tgcnaatcct gctggaggct 300
 gtcacacagg agatacactt tgtcaccttc tgtgccttcc agccctccc cagctgtctt 360
 cgcttcgtcc agaccaacat ctcccacctc ctgcaggaca cctcccagca gctggccgac 420
 ctgaagccct ggatcaccgc caggatttc tccgggtgac tggagctgca gtgtcagccc 480
 gactcctcta cattgggtgc cccaggagc ccgggggccc tggaggccac tgccttgcca 540
 gccctcagg cactcgggt gctcctcctg ctgctgctgc ccgtggctct cctgtgatg 600
 tccactgct ggtgcctgca ttggcgaagg aggggggggc ggaggtcac ctaccctggg 660
 gagcagagga cactgaggcc cagcagagcg agccatctgc ccgaggacac agagctggga 720
 cctggaggga gtcagctaga gactgttccc ttctcgacc agcagccccc gctcgtctcc 780
 tcccaggat caaggcaacg cccgccccca acgccccca agccagcccc agccccacct 840
 ctccccctct gtacaaagtc cttgccccca agaaattgta ta 882

<210> 10

<211> 882

<212> DNA

<213> Canis familiaris

<400> 10

tatacaattt cttgggggga aggaatttgt acaggggggg agaggtgggg ctggggctgg 60
 ctttgggggc gtggggggcg ggcgttgctt tgatcctggg gaggagagca ggggggctgc 120
 gtggtcgagg aagggaaccag tctctagctg actccctcca ggtcccagct ctgtgtcttc 180
 gggcagatgg ctccgtctgc tgggcctcag tgtcctctgc tcccaggggt aggggtgacct 240
 ccgcagccgc ctcccttcgc aatgcaggca ccaggcagtg gacatcagca ggagagccac 300
 gggcagcagc agcaggagga gcagccgagg tgccctgagg gctggcagag cagtggcttc 360
 cagggccccc gggctccttg ggggcaccaa tctagaggag tgggctgac actgcagctc 420
 caggcaccgc gagaaattcc tgcgggtgat ccagggtctc agggcggcca gctgctggga 480
 gctgtcctgc agggagtggg agatgttggt ctggacgaag cgaagcagc tggggagggg 540

ctggaaggca cagaaggtga caaagtgtat ctccgtgttg scagcctcca gcaggatttg 600
 catttgggat ccagccacag cctggagccg caccatccag cgtctggcca ggaccaggcg 660
 ccagaacgcc ccgcagagct cgtcgtcctg caggttggag gcgacagtga ctggatagtc 720
 ctgaagcagg taatcagaca gtttgccgat ggtgaccgag aaggtggagg agatggggct 780
 gtggctgag gagcagtcgg ggtcccgcg gaggccgggg ctgagcagca gcagcagcaa 840
 cagggaggca gttgggctcc aggctggcgc cagcactatc at 882

<210> 11

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 11

ctattaatgg gtctcacctc ccaact

26

<210> 12

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 12

tcaactcggg gcacagagtc ttgg

24

<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 13

ctgggeccag cctggagccc

20

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 14

gggggatgtt ggtctggacc

20

<210> 15

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 15

gaccaggcgc cagaccgc

18

<210> 16

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 16

cggtcccat ccgcaagc

18

<210> 17

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 17

tggcaaggca gtggcctc

18

<210> 18

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 18

gccgagatga tagtgcctggc

20

<210> 19

<211> 324

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(324)

<400> 19

cat aac ttc aat att act att aaa gag atc atc aaa atg ttg aac atc 48
His Asn Phe Asn Ile Thr Ile Lys Glu Ile Ile Lys Met Leu Asn Ile
1 5 10 15

ctc aca gcg aga aac gac tcg tgc atg gag ctg act gtc aag gac gtc 96
Leu Thr Ala Arg Asn Asp Ser Cys Met Glu Leu Thr Val Lys Asp Val
20 25 30

ttc act gct cca aag aac acc agc gat aag gaa atc ttc tgc aga gct 144
Phe Thr Ala Pro Lys Asn Thr Ser Asp Lys Glu Ile Phe Cys Arg Ala
35 40 45

gct act gta ctg cgg cag atc tat aca cac aac tgc tcc aac aga tat 192
Ala Thr Val Leu Arg Gln Ile Tyr Thr His Asn Cys Ser Asn Arg Tyr
50 55 60

etc aga gga etc tac agg aac etc agc agc atg gca sac aag acc tgt 240
 Leu Arg Gly Leu Tyr Arg Asn Leu Ser Ser Met Ala Asn Lys Thr Cys
 65 70 75 80

tct atg aat gaa etc aag aag agt aca ctg aas gac ttc ttg gaa agg 288
 Ser Met Asn Glu Ile Lys Lys Ser Thr Leu Lys Asp Phe Leu Glu Arg
 85 90 95

cta aaa gtg atc atg cag aag aaa tac tac agg cat 324
 Leu Lys Val Ile Met Gln Lys Lys Tyr Tyr Arg His
 100 105

<210> 20

<211> 108

<212> FRT

<213> Canis familiaris

<400> 20

His Asn Phe Asn Ile Thr Ile Lys Glu Ile Ile Lys Met Leu Asn Ile
 1 5 10 15

Leu Thr Ala Arg Asn Asp Ser Cys Met Glu Leu Thr Val Lys Asp Val
 20 25 30

Phe Thr Ala Pro Lys Asn Thr Ser Asp Lys Glu Ile Phe Cys Arg Ala
 35 40 45

Ala Thr Val Leu Arg Gln Ile Tyr Thr His Asn Cys Ser Asn Arg Tyr
 50 55 60

Leu Arg Gly Leu Tyr Arg Asn Leu Ser Ser Met Ala Asn Lys Thr Cys
 65 70 75 80

Ser Met Asn Glu Ile Lys Lys Ser Thr Leu Lys Asp Phe Leu Glu Arg
 85 90 95

Leu Lys Val Ile Met Gln Lys Lys Tyr Tyr Arg His
 100 105

<210> 21

<211> 324

<212> DNA

<213> Canis familiaris

<400> 21

atgcctgtag tctttcttct gcatgatcac ttttagcctt tccaagaggt ctttcagtggt 60

actcttcttg atttcattca tagaacaggt cttgtttgcc atgctgctga ggttcttgta 120
 gagtctcttg agtatcttgt tggagcagtt gtgtgtatag atctgccgca gtacagttagc 180
 agctctgcag aagatttcc tctcgtttgt gttctttgga gcagtgaaga cgtccttgac 240
 agtcagctcc atgcacaggt cgtttctcgc tgtgaggatg ttcaacattt tgaatgatctc 300
 ttttaatagta atattgaagt tatg 324

<210> 22

<211> 804

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(804)

<400> 22

acc ccc gac tgc tcc ttc agc cac agc ccc atc tcc tcc acc ttc ggc 48
 Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Ala
 1 5 10 15

gtc acc atc cgc aag ctg tot gat tac ctg ctt cag gac tat cca gtc 96
 Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val
 20 25 30

act gtc gcc tcc aac ctg cag gac gac gag ctc tgc ggg ggc ttc tgg 144
 Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp
 35 40 45

cgc ctg gtc ctg gcc cag cgc tgg atg gtg cgg ctc cag gct gtg gct 192
 Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala
 50 55 60

gga tcc caa atg caa atc ctg ctg gag gct gtc aac acg gag ata cac 240
 Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His
 65 70 75 80

ttt gtc acc ttc tgt gcc ttc cag ccc ctc ccc agc tgt ctt cgc ttc 288
 Phe Val Thr Phe Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe
 85 90 95

gtc cag acc aac atc tcc cac ctc ctg cag gac acc tcc cag cag ctg 336
 Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Gln Gln Leu

100	105	110	
gac gcc ctg aag ccc tgg atc acc cgc agg aat ttc tcc ggg tgc ctg			384
Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asp Phe Ser Gly Cys Leu			
115	120	125	
gag ctg cag tgt cag ccc gac tcc tct acc ttg gtg ccc cca agg agc			432
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser			
130	135	140	
ccc ggg gcc ctg gag gcc act gcc ttg cca gcc cct cag gca cct cgg			480
Pro Gly Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg			
145	150	155	160
ctg ctc ctc ctg ctg ctg ctg ccc gtg get ctc ctg ctg atg tcc act			528
Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Thr			
165	170	175	
gcc tgg tgc ctg cat tgg cga agg agg cgg cgg cgg agg tca ccc tac			576
Ala Trp Cys Leu His Trp Arg Arg Arg Arg Arg Arg Arg Ser Pro Tyr			
180	185	190	
cct ggg gag cag agg acc ctg agg ccc agc gag cgg agc cat ctg ccc			624
Pro Gly Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro			
195	200	205	
gag gac acc gag ctg gga cct gga ggg agt cag cta gag act ggt ccc			672
Glu Asp Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro			
210	215	220	
ttc ctc gac cac gca gcc cgg ctc get ccc tcc cca gga tca agg caa			720
Phe Leu Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln			
225	230	235	240
cgc cgg ccc cca acg ccc cca aag cca gcc cca gcc cca cct ctc ccc			768
Arg Pro Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro			
245	250	255	
ctc tgt acc aag tcc ttg ccc cca aga aat tgt eta			804
Leu Cys Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile			
260	265		

<210> 23

<211> 260

<212> PRT

<213> Canis familiaris

<400> 23

Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Ala
1 5 10 15

Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val
20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp
35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala
50 55 60

Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His
65 70 75 80

Phe Val Thr Phe Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe
85 90 95

Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Gln Gln Leu
100 105 110

Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu
115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser
130 135 140

Pro Gly Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg
145 150 155 160

Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Thr
165 170 175

Ala Trp Cys Leu His Trp Arg Arg Arg Arg Arg Arg Arg Ser Pro Tyr
180 185 190

Pro Gly Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro
195 200 205

Glu Asp Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro
210 215 220

Phe Leu Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln
225 230 235 240

Arg Pro Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro
245 250 255

Leu Cys Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile
 260 265

<210> 24

<211> 804

<212> DNA

<213> Canis familiaris

<400> 24

tatacaattt cttgggggca aggaactttgt acagaggggg agaggtgggg ctggggctgg 60
 ctttgggggc gttggggggc ggcgttgct tgatcctggg gaggagcga gcggggctgc 120
 gtggtcggg aggggaccag tctctagctg actccctcca ggtccagct ctgtgtcttc 180
 gggcagatgg ctccgctcgc tgggctcag tgcctctgc tcccagggg aggtgacct 240
 ccgcgcgcgc ctcttcgcc atgcaggca ccaggcagt gacatcaga ggagagccac 300
 gggcagcaga agcaggagga gcagccgagg tgctgaggg gctggcaagg cagtggcttc 360
 caggggcccc gggctccttg ggggcacca tgtagaggag tcgggtgac actgcagctc 420
 caggcaccgc gagaaattcc tgcgggtgat ccagggttc agggcggcca gctgctggga 480
 ggtgtcctgc aggggtggg agatgttgg ctggacgaag cgaagacaga tggggagggg 540
 ctggaaggca cagaaggtga caagtgat ctccgtgttg acagctcca gcaggatttg 600
 catttgggt ccagccacag cctggagccg caccatccag cgtggggcca ggaccaggcg 660
 ccagaacgcc ccgcagagct cgtcgtctc caggttgga ggcacagtga ctggatagtc 720
 ctgaagcagg taatcagaca gcttgccgat ggtgcccgc aaggtggagg agatggggct 780
 gtggctgag ggcagtcgg gggc 804

<210> 25

<211> 985

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (74)..(901)

<400> 25

ccggccctggc cccttccacg cccagctggg gcaagccctga tctgaccata ggcctgaggg 60

gcctccggcc gag atg ata gtg ctg gcg cca gcc tgg agc cca act gcc 109

Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Ala

1

5

10

tcc ctg ttg ctg ctg ctg ctg ctg agc ccc ggc ctg cgc ggg acc ccc 157

Ser Leu Leu Leu Leu Leu Leu Leu Ser Pro Gly Leu Arg Gly Thr Pro

15

20

25

gac tgc tcc ttc agc cac agc ccc atc tcc tcc acc ttc gcg gtc acc 205

Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Ala Val Thr

30

35

40

atc cgc aag ctg tct gat tac ctg ctt cag gac tat cca gtc act gtc 253

Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val

45

50

55

60

gcc tcc aac ctg cag gac gac gag ctg tgc ggg ggc ttc tgg cgc ctg 301

Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp Arg Leu

65

70

75

gtc ctg gcc cag cgc tgg atg gtg cgg ctg cag gct gtg gct gga tcc 349

Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala Gly Ser

80

85

90

caa atg caa atc ctg ctg gag gct gtc aac acc gag ata cac ttt gtc 397

Gln Met Gln Ile Leu Leu Glu Ala Val Asp Thr Glu Ile His Phe Val

95

100

105

acc ttc tgt gcc ttc cag gac acc tcc cag cag ctg gcc gcc ctg aag 445

Thr Phe Cys Ala Phe Gln Asp Thr Ser Gln Gln Leu Ala Ala Leu Lys

110

115

120

ccc tgg atc acc cgc agg aat ttc tcc ggg tgc ctg gag ctg cag tgt 493

Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu Gln Cys

125

130

135

140

cag ccc gac tcc tct acc ttg gtg ccc cca agg agc ccc ggg gcc ctg 541

Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser Pro Gly Ala Leu

145

150

155

gag gcc act gcc ttg cca gcc cct cag gcc cct cgg ctg ctg ctg ctg 589

Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu Leu Leu

160

165

170

ctg ctg ctg ccc gtg gct ctc ctg ctg atg tcc act gcc tgg tgg ctg 637
 Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Thr Ala Trp Cys Leu
 175 180 185

cat tgg cga agg agg cgg cgg cgg agg tca ccc tac cct ggg gag cag 665
 His Trp Arg Arg Arg Arg Arg Arg Arg Ser Pro Tyr Pro Gly Glu Gln
 190 195 200

agg aca ctg agg ccc agc gag cgg agc cat ctg ccc gag gac aca gag 733
 Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro Glu Asp Thr Glu
 205 210 215 220

ctg gga cct gga ggg agt cag cta gag act ggt ccc ttc ctc gac cac 781
 Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu Asp His
 225 230 235

gca gcc ccg ctc gct ccc tcc cca gga tca agg caa cgc ccg ccc cca 829
 Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro Pro Pro
 240 245 250

acg ccc cca aag cca gcc cca gcc cca cct ctc ccc ctc tgt aca aag 877
 Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro Leu Cys Thr Lys
 255 260 265

tcc ttg ccc cca aga aat tgt ata taaatcatcc tttttatccc gcaaaanaaa 931
 Ser Leu Pro Pro Arg Asn Cys Ile
 270 275

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 985

<210> 26

<211> 276

<212> PRT

<213> Canis familiaris

<400> 26

Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Ala Ser Leu Leu Leu
 1 5 10 15

Leu Leu Leu Leu Ser Pro Gly Leu Arg Gly Thr Pro Asp Cys Ser Phe
 20 25 30

Ser His Ser Pro Ile Ser Ser Thr Phe Ala Val Thr Ile Arg Lys Leu
 35 40 45

Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
 50 55 60

Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp Arg Leu Val Leu Ala Gln
 65 70 75 80
 Arg Trp Met Val Arg Leu Gln Ala Val Ala Gly Ser Gln Met Gln Ile
 85 90 95
 Leu Leu Glu Ala Val Asn Thr Glu Ile His Phe Val Thr Phe Cys Ala
 100 105 110
 Phe Gln Asp Thr Ser Gln Gln Leu Ala Ala Leu Lys Pro Trp Ile Thr
 115 120 125
 Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser
 130 135 140
 Ser Thr Leu Val Pro Pro Arg Ser Pro Gly Ala Leu Glu Ala Thr Ala
 145 150 155 160
 Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu Leu Leu Leu Leu Leu Pro
 165 170 175
 Val Ala Leu Leu Leu Met Ser Thr Ala Trp Cys Leu His Trp Arg Arg
 180 185 190
 Arg Arg Arg Arg Arg Ser Pro Tyr Pro Gly Glu Gln Arg Thr Leu Arg
 195 200 205
 Pro Ser Glu Arg Ser His Leu Pro Glu Asp Thr Glu Leu Gly Pro Gly
 210 215 220
 Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu Asp His Ala Ala Pro Leu
 225 230 235 240
 Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro Pro Pro Thr Pro Pro Lys
 245 250 255
 Pro Ala Pro Ala Pro Pro Leu Pro Leu Cys Thr Lys Ser Leu Pro Pro
 260 265 270
 Arg Asn Cys Ile
 275

<210> 27

<211> 985

<212> DNA

<213> Canis familiaris

<400> 27

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 ttgctggtag aaaaggatga ttatatata atttcttggg ggcaaggact ttgtacagag 120
 ggggagaggt ggggctgggg ctggttttgg gggtgttggg gggtgggttt gcttggatcc 180
 tggggagggg gggagggggg ctggttgggc gaggaaggga ccagtcctta gctgactccc 240
 tccaggtccc agctctgtgt cctcggggcag atgggtccgc tggctgggac tcagtgtcct 300
 ctgctcccca ggttaggggtg acctccggcg ccgtctctt cggcaatgca ggcaccaggg 360
 agtggacatc agcaggagag ccacggggcag cagcagcagg aggagcagcc gaggtgcttg 420
 aggggttggc aaggcagtgg cctccagggc cccggggctc cttgggggca ccaatgtaga 480
 ggggtcgggc tgacctgca gctccaggca cccggagaaa ttcttggggg tgatccaggg 540
 cttcaggggc gccagctgct gggagggtgc ctggaaggca cagaagggtg caaagtgtat 600
 ctccgtgttg acagctcca gaggatttg catttgggat ccagccacag cctggggccg 660
 caccatccag cgttgggcca ggcaccaggc ccagaacgac ccgcagagct cgtcgtcctg 720
 caggttggag ggcacagtga ctggatagtc ctgaagcagg taatcagaca gcttggggat 780
 ggtgaccgag aagggtggag agatggggct gtggctgaag gacagtcgg ggttcccgag 840
 gaggccgggg ctgagcgca gcagcagcaa caggggagga gtggggctcc aggttgggcg 900
 cagcactatc atctcggccg gaggcccttc atgcttatgg tcagatcagg cttgccccag 960
 ctgggcttgg aaggggccag gcccg 985

<210> 28

<211> 828

<212> DNA

<213> Canis familiaris

<400> 28

atgatatgtc tggcgccagc ctggggccca actgctccc tgttggctgt gctgtgtctc 60
 agccccggcc tccgggggac ccccgactgc tcttcagcc acagccccat ctctccacc 120
 ttgggggtca ccctccgcaa gctgtctgat tacctgttc aggaatatcc agtcactgtc 180

gctccaacc tgcaggacga cgagctctgc ggggagttat ggcgcctggc cctgggccag 240
 cgctggatgg tgcggctcca ggcgttggtt ggateccaaa tgcgaatcct gctggagggt 300
 gtcaacacgg agatacaatt tgtcaacctc tgtgccttcc aggacacctc ccagcagctg 360
 gccgccctga agccctggat caccgcaggg aatttctccg ggtgcctgga gctgcagtgt 420
 cagcccgact cctctacatt ggtgccccca aggagccccg gggccctgga ggcactgccc 480
 ttgccagccc ctccaggacc tcggctgttc ctctgtctgc tgcctgccgt ggctctcctg 540
 ctgatgtcca ctgcctgggt cctgcatttg cgaaggaggc ggcggcggaq gtcacctac 600
 cctggggagc agaggacact gaggccagc gaggcgagcc atctgccga ggcacagag 660
 ctgggacctg gagggagtcg gctagagact ggtcccttcc tgcaccagc agccccgtc 720
 gctccctccc caggatcag gcaagcccg ccccaacgc ccccaagcc agccccagc 780
 ccacctctcc cctctgtac aaagtcttg ccccaagaa attgtata 828

<210> 29

<211> 828

<212> DNA

<213> Canis familiaris

<400> 29

tatacaattt cttgggggga aggaatttgt acaagggggg agaggtgggg ctggggctgg 60
 ctttgggggc gttgggggag ggcgttgcct tgatcctggg gaggggagca ggcgggctgc 120
 gtggtcaggg aaggggaccag totctagctg actccctcca ggtcccaact ctgtgtctc 180
 gggcagatgg ctccgtctgc tgggcctcag tgcctcttgc tcccaggggt agggtgacct 240
 ccgcgcgcgc ctctttgcgc aatgcaggca ccaggcagtg gcatcagca ggaagaccac 300
 gggcagcagc agcaggagga gcagccgagg tgcctgaggg gctggcaggg cagtggctc 360
 caggggcccc ggcctccttg ggggcaccaa tctagaggag tcgggctgac actgcagctc 420
 caggcaccgc gagaatttc tgcgggtgat ccagggttc agggcggccg gctgctggga 480
 ggtctcttg aaggcacaga aggtgacaa gtgtctctcc gtgttgcag cctccagcag 540

gatttgatt tgggatccag ccacagcctg gagccgcacc atccagcgtt gggccaggac 600
 caggccccag aacgccccgc agagctcgtc gtcttgtagg ttggaggcca cagtgaactgg 650
 atagtcctga agcaggtaat cagacagctt gcggatgggt accgcgaagg tggaggagat 720
 ggggtgtgg ctgaaggagc agtcgggggt cccgaggagg ccggggctga gcagcagcag 780
 cagcaaccgg gaggcagttg ggctccaggc tggcgcacgc actatcat 828

<210> 30

<211> 750

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> {1}..(750)

<400> 30

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 Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Ala
 1 5 10 15

gtc acc atc cgc aag ctg tct gat tac ctg ctt cag gac tat cca gtc 96
 Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val
 20 25 30

act gtc gcc tcc aac ctg cag gac gac gag ctc tgc ggg ggc ttc tgg 144
 Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp
 35 40 45

cgc ctg gtc ctg gcc cag cgc tgg atg gtg cgg ctc cag gct gtg gct 192
 Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala
 50 55 60

gga tcc caa atg caa atc ctg ctg gag gct gtc aac acg gag ata cac 240
 Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asp Thr Glu Ile His
 65 70 75 80

ttt gtc acc ttc tgt gcc ttc cag gac acc tcc cag cag ctg gcc gcc 288
 Phe Val Thr Phe Cys Ala Phe Gln Asp Thr Ser Gln Gln Leu Ala Ala
 85 90 95

ctg aag ccc tgg atc acc cgc agg aat ttc tcc ggg tgc ctg gag ctg 336
 Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu
 100 105 110

cag tgt cag ccc gac tcc tct aca ttg gtg ccc cca agg agc ccc ggg 384
 Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser Pro Gly
 115 120 125

gcc ctg gag gcc act gcc ttg cca gcc cct cag gca cct cgg ctg ctc 432
 Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu
 130 135 140

ctc ctg ctg ctg ctg ccc gtg gct ctc ctg ctg atg tcc act gcc tgg 480
 Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Thr Ala Trp
 145 150 155 160

tgc ctg cat tgg cga agg agg cgg cgg cgg agg tca ccc tac cct ggg 528
 Cys Leu His Trp Arg Arg Arg Arg Arg Arg Arg Ser Pro Tyr Pro Gly
 165 170 175

gag cag agg eca ctg agg ccc agc gag cgg agc cat ctg ccc gag gac 576
 Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro Glu Asp
 180 185 190

aca gag ctg gga cct gga cgg agt cag cta gag act ggt ccc ttc ctc 624
 Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu
 195 200 205

gac cac gca gcc cgg ctc gct ccc tcc cca gga tca agg caa cgc ccg 672
 Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro
 210 215 220

ccc cca acg ccc cca aag cca gcc cca gcc cca cct ctc ccc ctc tgt 720
 Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro Leu Cys
 225 230 235 240

eca aag tcc ttg ccc cca aga aat tgt ata 750
 Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile
 245 250

<210> 31
 <211> 250
 <212> PRT
 <213> Canis familiaris

<400> 31
 Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Ala
 1 5 10 15

Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val

	20	25	30
Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp	35	40	45
Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala	50	55	60
Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His	65	70	75 80
Phe Val Thr Phe Cys Ala Phe Gln Asp Thr Ser Gln Gln Leu Ala Ala	85	90	95
Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu	100	105	110
Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser Pro Gly	115	120	125
Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu	130	135	140
Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Thr Ala Trp	145	150	155 160
Cys Leu His Trp Arg Arg Arg Arg Arg Arg Arg Ser Pro Tyr Pro Gly	165	170	175
Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro Glu Asp	180	185	190
Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu	195	200	205
Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro	210	215	220
Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro Leu Cys	225	230	235 240
Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile	245	250	

<210> 32

<211> 750

<212> DNA

<213> *Canis familiaris*

<400> 32

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 ctttgggggc gtgggggscg ggcgttgct tgcctctggg gagggagcga gggggctgc 120
 gtggtcgagg aagggaccag tctctagctg actcctcca ggtcccagct ctgtgtctc 180
 gggcagatgg ctccgctgc tgggcctcag tgctctctgc tcccaggggt agggtgacct 240
 ccgcgcgcgc ctctctgcgc aatgcaggca ccaggcagtg gacatcagca ggagagccac 300
 gggcagcagc agcaggagga gcagccgagg tgcttgaggg gctggcaagg cagtggcctc 360
 cagggccccg gggctccttg ggggcacca tgtagaggag tcgggctgac actgcagctc 420
 caggcaccgc gagaaattcc tgcgggtgat ccagggttc agggcggcca gctgctggga 480
 ggtgtcctgg aaggcacaga aggtgacaaa gtgtatctcc gtgttgacag cctccagcag 540
 gatttgcat tgggatccag ccacagcctg ggcgcgcacc atccagcgtt gggccaggac 600
 caggcgccag aacgccccgc agagctcgtc gtctgcagg ttggaggcga cagtgactgg 660
 atagtctga agcaggtaat cagacagctt gggatggtg accgcgaagg tggaggagat 720
 ggggctgtgg ctgaaggagc agtcgggggt 750

<210> 33

<211> 1019

<212> DNA

<213> *Canis familiaris*

<220>

<221> CDS

<222> (74)..(166)

<400> 33

ccggcctggc ccttccacg cccagctggg gcaagcctga tctgaccata ggcatgaggg 60
 gctccgggc gag atg ata gtg ctg gcg cca gcc tgg agc cca act gtg 109
 Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Val
 1 5 10
 cgt ata ccc ggg gga caa ggc ggg gga cag gca gag cgc tac cga gct 157
 Arg Ile Pro Gly Gly Gln Gly Gly Gly Gln Ala Glu Arg Tyr Arg Ala

15

20

25

ggg cag agc tgagagagca gacggacaga ggcctccctg ttgctgctgc 206
Gly Gln Ser

30

tgtgtctcag ccccggcctc cgcgggaccc ccgactgtc cttcagccac agcccatct 266
cctccacctt cgcgggcacc atccgcaagc tgtctgatta cctgtctcag gactatccag 326
tcactgtcgc etccsacctg caggacgacg agctctgcgg ggcgttctgg cgcctggctc 386
tggccacagc ctggatggcg cggctccagg ctgtggctgg atcccaaatg caactcctgc 446
tggaggtctg caacacggag atacacttg tcaactctg tgccttcag gacacctcc 506
agcagctggc cgccttgagc ccttgatca cccgcaggaa ttctccggg tgcctggagc 566
tgcagtgtca gcccgactcc tctacattgg tgcctccaaag gaggcccggg gccctggagc 626
ccactgcctt gccagccctt caggcacctc ggcgtctcct cctgtgtctg ctgcccgtgg 686
ctctctgtct gatgtccact gccctggctc tgcattggcg aaggaggcgg cggcggaggt 746
caccctacc tggggagcag aggcactga ggcacagcga ggcgagccat ctgcccagag 806
acacagagct gggacctgga gggagtccgc tagagactgg tcccttctc gaccacgcag 866
ccccgtcgc tccctccca ggcacaggc aacgcccgc cccacgcgc ccaagccag 926
ccccagccc acctctccc ctctgtacaa agtccttgc cccagaaat tctatataa 986
tcctctttt ctacaaaaa aaaaaaaba aaa 1019

<210> 34

<211> 31

<212> PRT

<213> Canis familiaris

<400> 34

Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Val Arg Ile Pro Gly
1 5 10 15

Gly Gln Gly Gly Gly Gln Ala Glu Arg Tyr Arg Ala Gly Gln Ser
20 25 30

<210> 35
 <211> 1019
 <212> DNA
 <213> Canis familiaris

<400> 35
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 accttgtaca gagggggaga ggtggggctg gggctggctt tgggggctt gggggcgggc 120
 gttgccttga tcttggggag ggagcgagcg gggctggctg gtcgaggag ggaccagtct 180
 ctgctgact cctccagggt cccagctctg tgtctcggg cagatggctc cgtcgtctgg 240
 gctcagtggt cctctgtctc ccagggtagg gtgacctcg ccgcccctc cttcgccaat 300
 gcaggcacca ggcagtggac atcagcagg gggccacggg cagcagcagc aggaggggca 360
 gcagaggtgc ctgaggggct ggcagggcag tggcctccag ggccccgggg ctcttgggg 420
 gcaccaatgt agaggagtcg ggctgacct gcagctccag gcaccggag aatkcctgc 480
 gggatgacca gggcttcagg gcggccagct gctgggaggt gtcctggag gcacagagg 540
 tgacaaagtg tatctcgtg ttgacagcct ccagcaggat ttgcatttgg gatccagcca 600
 cagcctggag ccgcaccatc cagcgttggg ccaggaccag gcggcagAAC gccccgaga 660
 gctcgtctc ctgcaggttg gaggcgacag tgaactggata gtctgaagc aggtaatcag 720
 acagcttgcg gatggtgacc gcgaggttg aggagatggg gctgtggctg aaggagcagt 780
 cgggggtccc ggggagggcg gggctgagca gcagcagcag caacaggggg gcctctgtcc 840
 gtctgtctc tcagctctgc ccagctcgggt agcgtctctc ctgtccccg ccttgtcccc 900
 cgggtatccg cacagttggg ctccaggttg gcgcagcac tatcatctcg gcggagggcc 960
 cctcatgcct atggtcagat caggcttgc ccagctgggc gtggaggggg ccaggccgg 1019

<210> 36
 <211> 93
 <212> DNA
 <213> Canis familiaris

<400> 36
 atgatagtgc tggcgccagc ctggagccca actgtgccta tccccgggg acaaggcggg 60

ggacaggcag agcgcaccg agctgggcag agc

93

<210> 37

<211> 93

<212> DNA

<213> Canis familiaris

<400> 37

gctctgccc gctcggtagc gctctgccc tccccgcct tgtccccgg gtatacgac 60

agttgggctc caggtggcg ccagcactat cat

93

<210> 38

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 38

tgaattcgga cataacttca atattac

27

<210> 39

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 39

tctcgagatt cagcttcaat gcctgta

27

<210> 40

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

Primer

<400> 40

cccaagctta tgggtctcac ctcccaac

28

<210> 41

<211> 395

<212> DNA

<213> Felis catus

<400> 41

ggccataggc atgaagggcc tccggccgag atgatatgtc tggcgccagc ctggagccca 60

actacctccc tgcctgtgct gctactgtct agccctggcc tccgggggtc cccgactgt 120

tccctcagcc acagcccccct ctctccacc ttcagggtca ccatccgaaa gctgtctgat 180

tacctgttc aggtattacc agtcaccgtc gcctccaaac tacaggacga cgagctctgt 240

gggcattct ggcacctggt cctggcccag cgtgggatgg gtccgctcaa ggcctgtggt 300

gggtcccaga tgc aaagcct gctggaggcg gtcaacaccg agatacattt tgtcaccttg 360

tgtgccttc agccctccc cagctgtctt cgatt 395

<210> 42

<211> 793

<212> DNA

<213> Felis catus

<400> 42

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cgctccaac ctacaggacg acgagctctg tgggcattc tggcacctgg tctggccca 120

ggcctggatg ggtccgctca aggtgtgtgc tgggtcccag atgc aaagcc tgcctggaggc 180

ggtcacacc gagatacatt ttgtcacctt gtgtgccttc cagccctcc cccgctgtct 240

tcgattcgtc cagaaccaaa tctccacct cctgcaggac acctccgagc agctggccgc 300

cttgaagccc tggatcacc gcaggaaatt ctgggggtgc ctggagctac agtctcagcc 360

cgaetctcc accccaactgc ccccaaggag ccccaaggcc ttggaggcca cagccctgcc 420

agccctcag gccctctgc tgcctctct gctgtgttg cctgtggctc tcttctgat 480

gtccgccgcc tggcgccctgc actggcgagag saggagatgg agaacgccct accccaggga 540
gcagaggagag acactgaggg ccagagagag gaatcacctg ccgaggagca cagagccggg 600
actcggagaa agtcagctag agactgggtt ctctctcgac cagctgccc cgtcactct 660
ccccccggga tggaggcaac gccagccccc aacgccagcc ccagaccac ctatccccct 720
ctgtacaaag tccttgctct caggaaattg tatataata atccttttct accaaaaaa 780
aaaaaaaaaaa aaa 793

<210> 43
<211> 942
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (31)..(903)

<400> 43
ggccatagga atgaagggcc tccggccgag atg ata gtg ctg gag cca gcc tgg 54
Met Ile Val Leu Ala Pro Ala Trp
1 5

agc cca act acc tcc ctg ctg ctg ctg cta ctg ctg agc cct ggc ctg 102
Ser Pro Thr Thr Ser Leu Leu Leu Leu Leu Leu Leu Ser Pro Gly Leu
10 15 20

ggc ggg tcc ccc gac tgt tcc ttc agc ccc agc ccc atc tcc tcc acc 150
Arg Gly Ser Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr
25 30 35 40

ttc aag gtc acc atc cga aag ctg tct gat tac ctg ctt cag gat tac 198
Phe Lys Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr
45 50 55

cca gtc acc gtc gcc tcc aac cta cag gac gac gag ctg tgt ggg cca 246
Pro Val Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Pro
60 65 70

ttc tgg cac ctg gtc ctg gcc cag cgc tgg atg ggt cgg ctg aag gct 294
Phe Trp His Leu Val Leu Ala Gln Arg Trp Met Gly Arg Leu Lys Ala
75 80 85

gtg gct ggg tcc cag atg caa agc ctg ctg gag gcg gtc aac acc gag 342
 Val Ala Gly Ser Gln Met Gln Ser Leu Leu Glu Ala Val Asn Thr Glu
 90 95 100

ata cat ttt gtc acc ttg tgt gcc ttc cag ccc ctc ccc agc tgt ctt 390
 Ile His Phe Val Thr Leu Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu
 105 110 115 120

cga ttc gtc cag acc aac atc tcc cac ctc ctg cag gac acc tcc gag 438
 Arg Phe Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Glu
 125 130 135

cag ctg gcg gcc ttg aag ccc tgg atc acc cgc agg aat ttc tcg ggg 486
 Gln Leu Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly
 140 145 150

tgc ctg gag cta cag tgt cag ccc gac tcc tcc acc cca ctg ccc ccc 534
 Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Pro Leu Pro Pro
 155 160 165

agg agc ccc agg gcc ttg gag gcc aca gcc ctg cca gcc cct cag gcc 582
 Arg Ser Pro Arg Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala
 170 175 180

cct ctg ctg ctc ctc ctg ctg ctg ttg cct gtg gct ctc ttg ctg atg 630
 Pro Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met
 185 190 195 200

tcc gcc gcc tgg tgc ctg cac tgg cga aga agg aga tgg aga acg ccc 678
 Ser Ala Ala Trp Cys Leu His Trp Arg Arg Arg Arg Trp Arg Thr Pro
 205 210 215

tac ccc agg gag cag agg aag aca ctg agg ccc aga gag agg aat cac 726
 Tyr Pro Arg Glu Gln Arg Lys Thr Leu Arg Pro Arg Glu Arg Asn His
 220 225 230

ctg ccc gag gac aca gag ccg gga ctc gga gaa agt cag cta gag act 774
 Leu Pro Glu Asp Thr Glu Pro Gly Leu Gly Glu Ser Gln Leu Glu Thr
 235 240 245

ggt tcc ttc ctc gac cac gct gcc ccg ctc act ctc ccc ccg gga tgg 822
 Gly Ser Phe Leu Asp His Ala Ala Pro Leu Thr Leu Pro Pro Gly Trp
 250 255 260

agg caa cgc cag ccc cca acg cca gcc cca gac cca cct atc ccc ctc 870
 Arg Gln Arg Gln Pro Pro Thr Pro Ala Pro Asp Pro Pro Ile Pro Leu
 265 270 275 280

tgt aca aag tcc ttg tcc tca gga aat tgt ata taatcatcc ttttctacca 923
 Cys Thr Lys Ser Leu Ser Ser Gly Asn Cys Ile
 285 290

aaaaaaaaaa aaaaaaaaaa

942

<210> 44

<211> 291

<212> PRT

<213> Felis catus

<400> 44

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 1 5 10 15
 Leu Leu Leu Leu Ser Pro Gly Leu Arg Gly Ser Pro Asp Cys Ser Phe
 20 25 30
 Ser His Ser Pro Ile Ser Ser Thr Phe Lys Val Thr Ile Arg Lys Leu
 35 40 45
 Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
 50 55 60
 Gln Asp Asp Gln Leu Cys Gly Pro Phe Trp His Leu Val Leu Ala Gln
 65 70 75 80
 Arg Trp Met Gly Arg Leu Lys Ala Val Ala Gly Ser Gln Met Gln Ser
 85 90 95
 Leu Leu Glu Ala Val Asn Thr Glu Ile His Phe Val Thr Leu Cys Ala
 100 105 110
 Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 115 120 125
 His Leu Leu Gln Asp Thr Ser Glu Gln Leu Ala Ala Leu Lys Pro Trp
 130 135 140
 Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu Gln Cys Gln Pro
 145 150 155 160
 Asp Ser Ser Thr Pro Leu Pro Pro Arg Ser Pro Arg Ala Leu Glu Ala
 165 170 175
 Thr Ala Leu Pro Ala Pro Gln Ala Pro Leu Leu Leu Leu Leu Leu Leu
 180 185 190

Leu Pro Val Ala Leu Leu Leu Met Ser Ala Ala Trp Cys Leu His Trp
195 200 205

Arg Arg Arg Arg Trp Arg Thr Pro Tyr Pro Arg Glu Gln Arg Lys Thr
210 215 220

Leu Arg Pro Arg Glu Arg Asn His Leu Pro Glu Asp Thr Glu Pro Gly
225 230 235 240

Leu Gly Glu Ser Gln Leu Glu Thr Gly Ser Phe Leu Asp His Ala Ala
245 250 255

Pro Leu Thr Leu Pro Pro Gly Trp Arg Gln Arg Gln Pro Pro Thr Pro
260 265 270

Ala Pro Asp Pro Pro Ile Pro Leu Cys Thr Lys Ser Leu Ser Ser Gly
275 280 285

Asn Cys Ile
290

<210> 45
<211> 942
<212> DNA
<213> Felis catus

<400> 45
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 ccattccggg gggagagtga ggggggcagc gtggtcaggg aaggaaccag tctctagctg 180
 acttctccg agtcccggt ctgtgtcttc gggcaggtag tctctcttc tgggcctcag 240
 tcttctcttc tgcctccctgg ggtagggcgt tctccatctc cttcttcgcc agtcaggcca 300
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 ggcctcgagg gctggcaggg ctgtggcttc caaggccctg gggctccttg ggggcagtgg 420
 ggtggaggag tcgggctgac actgtagctc caggcaccoc gagaaatttc tgcgggtgat 480
 ccagggttcc aaggccgcca gctgctcggg ggtgtcttcg aggaggtggg agatgttggt 540
 ctggacgaat cgaagacagc tggggagggg ctggaaggca cacaaggtag caaatgtat 600

ctgggtgttg accgctcca gcaggctttg catctgggac ccagccacag ccttgagccg 660
 scccatccag cgtctgggcca ggaccaggct ccagaatggc ccacagagct cgtctctctg 720
 taggttggag gcgacggtga ctgggtatc ctgaagcagg taccagaca gctttcggac 780
 ggtgaccttg aaggtggagg agatggggct ctggtgaaag gaacgtcggg gggaccgccc 840
 gaggcagggt ctgagcagta gcagcagcag caggaggtta gttgggctcc aggtcggccc 900
 cagcctatc atctgggccc gaggccttc atgcctatgg cc 962

<210> 46
 <211> 873
 <212> DNA
 <213> Felis catus

<400> 46
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 agccctggcc tccgggggtc ccccgactgt tcttccagcc acagcccat ctctccccc 120
 ttcaaggctca ccatccgaaa gctgtctgat taactgcttc aggattaccc agtcaccgctc 180
 gctccacccc tacaggagca cgagctctgt gggccattct ggcacctggc cctggcccaag 240
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 gccctcagg cccctctgt gctcctctg ctgctgttgc ctgtggctct cttgctgatg 600
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 caggggaga cactgaggcc cagagagagg atcacctgc ccaggagac agagccggga 720
 ctggagaaa gtcagctaga gactggctcc ttctcgacc agctgccc gctactctc 780
 ccccgggat ggaggcaacg ccagccccc acgcagccc cagaccacc tatccccctc 840

cgacaaagt ccttgctctc aggaattgt ata

813

<210> 47

<211> 873

<212> DNA

<213> Felis catus

<400> 47

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 gaaggaaaca gtctctagct gaatttctcc ggtcccggc tctgtgtcct cgggcagggtg 180
 attcctctct ctgggcctca gtgtttctct ctgtccctg gggtagggcg ttctccatct 240
 ccttcttcgc cagtgcaggc accaggcggc ggacatcagc aagagagcca caggcaacag 300
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 ggggtctctt gggggcagtg gggtaggaga gtggggctga cactgtagct ccaggcacc 420
 cgagaaattc ctgcgggtga tccagggctt caaggccgac agctgtcgg aggtgtcctg 480
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 cccagccaca gccttgagcc gaccatcca gcgtgggccc aggaaccaagt gccagaatgg 660
 cccacagagc tctgtgtcct gtaggttga ggcgacggtg actgggtaat cctgaagcag 720
 gtaatcagac agctttcggg tggtagcctt gaaggtggag gagatggggc tgtggctgaa 780
 ggaacagtcg ggggacccgc gggggccagg gctgagcagt agcagcagca gcaggaggt 840
 agttgggtc caggctggcg ccagcactat cat 873

<210> 48

<211> 795

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1) .. (795)

<400> 48

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Ser Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Lys	
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gtc acc atc cga aag ctg tct gat tac ctg ctt cag gat tac cca gtc	96
Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val	
20 25 30	
ccc gtc gcc tcc aac cta cag gac gac gag ctc tgt ggg cca ttc tgg	144
Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Pro Phe Trp	
35 40 45	
cac ctg gtc ctg gcc cag cgc tgg atg ggt cgg ctc aag gct gtg gct	192
His Leu Val Leu Ala Gln Arg Trp Met Gly Arg Leu Lys Ala Val Ala	
50 55 60	
ggg tcc cag atg cca agc ctg ctg gag ggc gtc aac acc gag ata cat	240
Gly Ser Gln Met Gln Ser Leu Leu Glu Ala Val Asn Thr Glu Ile His	
65 70 75 80	
ttt gtc acc ttg tgt gcc ttc cag ccc ctc ccc agc tgt ctt cga ttc	288
Phe Val Thr Leu Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe	
85 90 95	
gtc cag acc aac atc tcc cac ctc ctg cag gac acc tcc gag cag ctg	336
Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Glu Gln Leu	
100 105 110	
ggg gcc ttg aag ccc tgg atc acc cgc agg aat ttc tcc ggg tgc ctg	384
Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu	
115 120 125	
gag cta cag tgt cag ccc gac tcc tcc acc cca ctg ccc cca agg agc	432
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Pro Leu Pro Pro Arg Ser	
130 135 140	
ccc agg gcc ttg gag gcc aca gcc ctg cca gcc cct cag gcc cct ctg	480
Pro Arg Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Leu	
145 150 155 160	
ctg ctc ctc ctg ctg ctg ttg cct gtg gct ctc ttg ctg atg tcc gcc	528
Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Ala	
165 170 175	
gcc tgg tgc ctg cac tgg cga aga agg aga tgg aga acc ccc tac ccc	576
Ala Trp Cys Leu His Trp Arg Arg Arg Arg Trp Arg Thr Pro Tyr Pro	

180	185	190	
agg gag cag agg aag aca ctg agg ccc aga gag agg aat cac ctg ccc			624
Arg Glu Gln Arg Lys Thr Leu Arg Pro Arg Glu Arg Asn His Leu Pro			
195	200	205	
gag gac aca gag ccg gga ctc gga gaa agt cag cta gag act ggt tcc			672
Glu Asp Thr Glu Pro Gly Leu Gly Glu Ser Gln Leu Glu Thr Gly Ser			
210	215	220	
ttc ctc gac cac gat gcc ccg ctc act ctc ccc ccg gga tgg agg caa			720
Phe Leu Asp His Ala Ala Pro Leu Thr Leu Pro Pro Gly Trp Arg Gln			
225	230	235	240
ccg cag ccc cca acg cca gcc cca gac cca cct atc ccc ctc tgt aca			768
Arg Gln Pro Pro Thr Pro Ala Pro Asp Pro Pro Ile Pro Leu Cys Thr			
245	250	255	
aag tcc ttg tcc tca gga aat tgt ata			795
Lys Ser Leu Ser Ser Gly Asn Cys Ile			
260	265		

<210> 49

<211> 265

<212> PRT

<213> Felis catus

<400> 49

Ser	Pro	Asp	Cys	Ser	Phe	Ser	His	Ser	Pro	Ile	Ser	Ser	Thr	Phe	Lys
1				5					10					15	
Val	Thr	Ile	Arg	Lys	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val
			20					25					30		
Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Asp	Glu	Leu	Cys	Gly	Pro	Phe	Trp
			35				40					45			
His	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Gly	Arg	Leu	Lys	Ala	Val	Ala
		50				55					60				
Gly	Ser	Gln	Met	Gln	Ser	Leu	Leu	Glu	Ala	Val	Asn	Thr	Glu	Ile	His
		65				70				75				80	
Phe	Val	Thr	Leu	Cys	Ala	Phe	Gln	Pro	Leu	Pro	Ser	Cys	Leu	Arg	Phe
				85					90					95	
Val	Gln	Thr	Asn	Ile	Ser	His	Leu	Leu	Gln	Asp	Thr	Ser	Glu	Gln	Leu

	100	105	110
Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu			
115	120	125	
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Pro Leu Pro Pro Arg Ser			
130	135	140	
Pro Arg Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Leu			
145	150	155	160
Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Ala			
165	170	175	
Ala Trp Cys Leu His Trp Arg Arg Arg Arg Trp Arg Thr Pro Tyr Pro			
180	185	190	
Arg Glu Gln Arg Lys Thr Leu Arg Pro Arg Glu Arg Asn His Leu Pro			
195	200	205	
Glu Asp Thr Glu Pro Gly Leu Gly Glu Ser Gln Leu Glu Thr Gly Ser			
210	215	220	
Phe Leu Asp His Ala Ala Pro Leu Thr Leu Pro Pro Gly Trp Arg Gln			
225	230	235	240
Arg Gln Pro Pro Thr Pro Ala Pro Asp Pro Pro Ile Pro Leu Cys Thr			
245	250	255	
Lys Ser Leu Ser Ser Gly Asn Cys Ile			
260	265		

<210> 50

<211> 795

<212> DNA

<213> Felis catus

<400> 50

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gaaggaacca gtctctagct gactttctcc ggtcccggtc tctgtgtctt cgggcaggtg 180

attctctctt ctgggctcca gtgtcttctt ctgtccctg gggtaggggc ttctccatct 240

ccttcttgc cagtgcaggc accagggggc ggcattcagc aagagagcca caggcaacag 300

cagcaggagg agcagcagag gggcctgagg ggcaggcagg gctgtggcct ccaaggccct 360
 ggggtccctt gggggcagtg gggtagagga gtcgggctga cactgtagct ccaggcacc 420
 cgagaaattc ctgcgggtga tccaggcctt caaggccgcc agctgctcgg aggtgtcctg 480
 caggaggttg gagatgttgg tctggscgaa tcgaagacag ctggggaggg gctggagggc 540
 acacaaggtg acaaatgta tctcgggtgtt gscggcctcc agcaggcttt gcattctggga 600
 cccagccaca gcttgagcc gaccatcca gcgctgggccc aggaccaggt gccagaatgg 660
 ccacagagc tctcgtcctt gttaggttga ggcgacggtg actgggtaat cctgaagcag 720
 gtaatcagac agctttcggg tggtagcctt gagggtggag gagatggggc tgtggctgaa 780
 ggaacagtcg gggga 795

<210> 51
 <211> 321
 <212> DNA
 <213> *Canis familiaris*

<400> 51
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 gtgaagggtc aggcggggaac taacaagact gatgttatct gtggtcccca gcctcgggta 120
 agagccctag tggtaggtccc catcattatg gggatcctgc ttgttgtcct gttgggtgtc 180
 gcctgcaccc gaaagggtgg caagaagcca gagaataagg ttatgtatca ggaccctgtg 240
 gaggaacttg aggaatttcc tatgcccccg cactccattg ctccggtgca agagacctta 300
 catgggtgac agcccgtcac c 321

<210> 52
 <211> 1425
 <212> DNA
 <213> *Canis familiaris*

<220>
 <221> CDS
 <222> [196]..[1017]

tagactcccg ggaatattca ggggaactcc cgggcgttaa ggtctccagg agctccgcgg 60

ggggggggggc·aaagggctggg gaggttactaa agacatcccc ggcccctac tccgctgcct 160

Met Val Leu Leu Pro Leu Arg Cys Leu Phe Trp Gly

10

Ser Leu Leu Thr Thr Val Tyr Pro Glu Pro Arg Thr Ala Cys Arg Glu

25.

Lys Gln Tyr Leu Val Asp Ser Gln Cys Cys Asn Met Cys Pro Pro Gly

40

Glu Lys Leu Val Asn Asp Cys Leu His Thr Ile Asp Thr Glu Cys Thr

50

Arg Cys Gln Thr Gly Glu Phe Leu Asp Thr Trp Asn Ala Glu Arg His

75

Cys His Gln His Lys Tyr Cys Asp Pro Asn Leu Gly Leu His Val Glu

90

Lys Glu Gly Thr Ser Glu Thr Asp Thr Thr Cys Thr Cys Asp Glu Gly

105

Leu His Cys Thr Asn Ala Ala Cys Glu Ser Cys Thr Met His Ser Leu

120

Cys Pro Pro Gly Leu Gly Val Lys Gln Ile Ala Thr Gly Ile Ser Asp

140

Thr Ile Cys Asp Pro Cys Pro Ile Gly Phe Phe Ser Asn Val Ser Ser

155

gct ttc gaa aag tgt ccc cct tgg aca agc tgt gaa acc aaa ggc ctg

Ala Leu Glu Lys Cys His Pro Trp Thr Ser Cys Glu Thr Lys Gly Leu
 160 165 170

gtg aag gtt cag gcg gga act aac aag act gat gtt atc tgt ggt ccc 759
 Val Lys Val Gln Ala Gly Thr Asn Lys Thr Asp Val Ile Cys Gly Pro
 175 180 185

cag cct cgg tta aga gcc cta gtg gtg gtc ccc atc att atg ggg atc 807
 Gln Pro Arg Leu Arg Ala Leu Val Val Val Pro Ile Ile Met Gly Ile
 190 195 200

ctg ctt gtt gtc ctg ttg gtg tct gcc tgc atc cga aag gtg gtc aag 855
 Leu Leu Val Val Leu Leu Val Ser Ala Cys Ile Arg Lys Val Val Lys
 205 210 215 220

aag cca gag aat aag gtt atg tat cag gac cct gtg gag gac ttg gag 903
 Lys Pro Glu Asn Lys Val Met Tyr Gln Asp Pro Val Glu Asp Leu Glu
 225 230 235

gaa ttt cct atg ccc ccg cac tcc att gct ccg gtg caa gag acc tta 951
 Glu Phe Pro Met Pro Pro His Ser Ile Ala Pro Val Gln Glu Thr Leu
 240 245 250

cct ggg tgc cag ccc gtc acc cag gag gac ggc aaa gag agc cgc atc 999
 His Gly Cys Gln Pro Val Thr Gln Glu Asp Gly Lys Glu Ser Arg Ile
 255 260 265

tcc gtg cag gag agt gtg tgaggcagcg tgtgccacgg agtgtgacag 1047
 Ser Val Gln Glu Arg Val
 270

cgtgggagag tgggcgcgtg gctggagagc ctggagctgc tggaggggca tgaagggggc 1107

gtgtcccccct gctgcaccc ctgtgtctgc gaaacagaga accttcacc ccacccctgg 1167

agcccattcc acctcccaac ttgcttttaa agatggagat gaaacttttg ggggggccaga 1227

tagtaatatc caccaccca gcatttcagg gccctgaggt gtatatcag gtggttttata 1287

cgagcccagg aagaccncc agagaccatt gtcgcattgt ttgtgacagt ggacaactgg 1347

aggccactta gctgttcagc agcaggggac tggctaaata aaatttgtaa tataattata 1407

aaaaaaaaa aaaaaaaa 1425

<210> 53

<211> 274

<212> PRT

<213> *Canis familiaris*

<400> 53

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Thr Val Tyr Pro Glu Pro Arg Thr Ala Cys Arg Glu Lys Gln Tyr Leu
 20 25 30

Val Asp Ser Gln Cys Cys Asn Met Cys Pro Pro Gly Glu Lys Leu Val
 35 40 45

Asn Asp Cys Leu His Thr Ile Asp Thr Glu Cys Thr Arg Cys Gln Thr
 50 55 60

Gly Glu Phe Leu Asp Thr Trp Asn Ala Glu Arg His Cys His Gln His
 65 70 75 80

Lys Tyr Cys Asp Pro Asn Leu Gly Leu His Val Glu Lys Glu Gly Thr
 85 90 95

Ser Glu Thr Asp Thr Thr Cys Thr Cys Asp Glu Gly Leu His Cys Thr
 100 105 110

Asn Ala Ala Cys Glu Ser Cys Thr Met His Ser Leu Cys Pro Pro Gly
 115 120 125

Leu Gly Val Lys Gln Ile Ala Thr Gly Ile Ser Asp Thr Ile Cys Asp
 130 135 140

Pro Cys Pro Ile Gly Phe Phe Ser Asn Val Ser Ser Ala Leu Glu Lys
 145 150 155 160

Cys His Pro Trp Thr Ser Cys Glu Thr Lys Gly Leu Val Lys Val Gln
 165 170 175

Ala Gly Thr Asn Lys Thr Asp Val Ile Cys Gly Pro Gln Pro Arg Leu
 180 185 190

Arg Ala Leu Val Val Val Pro Ile Ile Met Gly Ile Leu Leu Val Val
 195 200 205

Leu Leu Val Ser Ala Cys Ile Arg Lys Val Val Lys Lys Pro Glu Asn
 210 215 220

Lys Val Met Tyr Gln Asp Pro Val Glu Asp Leu Glu Glu Phe Pro Met
 225 230 235 240

Pro Pro His Ser Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln
 245 250 255

Pro Val Thr Gln Glu Asp Gly Lys Glu Ser Arg Ile Ser Val Gln Glu
 260 265 270

Arg Val

<210> 54

<211> 1425

<212> DNA

<213> Canis familiaris

<400> 54

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 tgggtcttcc tgggctcgta gaaccacccg tgaratacac ctccaggccc tgaaatgctg 180
 ggttggtgga tattactatc tggcccccac aaagcttcat ctccatcttt aaaagcaagt 240
 tgggaggtgg aatgggctcc aggggtgggg tggagggtc tctgtttctg cagcacaggg 300
 gtgcaggcag gggagcaccg ccccttcctg cccctccagc agctccaggc tctccagcca 360
 cgcgccact ctcccacgt gtccactcc tgggcacccg ctgctcaca ctctctctg 420
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 gtctgatac ataacottat tctctggctt ctgaccacc tttaggatgc aggcagacac 600
 caacaggaca scaggcagga tcccataat gatggggacc accactaggg ctcttaaccg 660
 aggttgggga ccacagataa catnagtctt gttagtccc gctgaacct teaccaggcc 720
 ttgggttca cagcttctcc aagggtgaca cttttccaaa gcagagaca cattggagaa 780
 gaagccgatg gggcagggat cgcagatggt atcagaatc cctgtagcga tctgtttgac 840
 tccaggcca ggggggcaca ggotgtgcct ggtgcagctc tcacaggcag cgttggtaca 900
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 gaagagacag cgcagaggga ggagaacctt ggcgaggtga atagcaggca gcggagtagg 1260
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<210> 55

<211> 822

<212> DNA

<213> Canis familiaris

<400> 55

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 tgcaccaccg gagagaaact ggtgaatgac tgcctacata ccattgacac ggaatgcact 180
 cgttgccaaa caggcgaatt cctagacact tggagcgag agagacactg tcaccagcac 240
 aatatctgcg accccaacct agggctccat gtcgagaagg agggcagctc agaacacgac 300
 accacttgc catgcgatga aggtctgcat tgtaccaacg ctgcctgtga gagctgcacc 360
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 aagactgatg ttatctgtgg tcccagcct cggttaagag cctagtgtt ggtcccatc 600
 attatgggga tctgtctgt tgcctgttg gtgtctgct gcacccgaaa ggtggtcag 660
 aagccagagc ataaggttat gtatcaggac cctgtggagg acttgaggga atttctatg 720

ccccgcact ccattgctcc ggtgcaagag accttacatg ggtgocagcc cgtcaccacg 780

gaggccggca aagagagccg catctccgtg caggagagag tg 822

<210> 56

<211> 822

<212> DNA

<213> Canis familiaris

<400> 56

cactctctcc tgcacggaga tgcggctctc ttgctctcc tctgggtga cgggctggca 60

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gtctccaca gggctctgat acatacctt attctctgc tcttgacca ccttcggat 180

gcaggcagcc accaacagga cacaagcag gatcccata atgatggga ccaccactag 240

ggctcttaac cgggctggg gaccacagat aacatcagt ttgttagtgc cggctgaac 300

ctccaccagg ccttkggtt cacagctgt ccaagggtga cactkttcca aagcagaaga 360

cacattggag aagcagccga tggggcaggg atgcagatg gtatcagaa tccctgtagc 420

gatctgttg actccaggc caggggggca caggctgtgc atggkcgagc tctccaggc 480

agcgttgga caatgcagac ctccatcgca tgtgcaagt gtgtctgtt ctgctgtgc 540

ctccttctcg acatggagcc ctaggctggg gtgcagtat ttgtctggt gacagtgtct 600

ctctgcttc caagtgtct ggaatccgc tgtttggca cggkcgatt cgtgtcact 660

ggtatgtagg cagtcattca ccagttctc tctgggtgg cacatattac agcactgact 720

gtctactagg tattgcttt ctctgcatg agtgcgtgt tctgggtaga cggtggtcaa 780

caaggagccc cagaagagac agcgcagagg caggagzacc at 822

<210> 57

<211> 765

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(765)

<400> 57

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Pro Glu Pro Arg Thr Ala Cys Arg Glu Lys Gln Tyr Leu Val Asp Ser
1 5 10 15

cag tgc tgt aat atg tgc cca cca gga gag aaa ctg gtg aat gac tgc 96
Gln Cys Cys Asn Met Cys Pro Pro Gly Glu Lys Leu Val Asn Asp Cys
20 25 30

cta cat acc att gac acg gaa tgc act cgt tgc caa acc ggc gaa ttc 144
Leu His Thr Ile Asp Thr Glu Cys Thr Arg Cys Gln Thr Gly Glu Phe
35 40 45

cta gac act tgg aac gca gag aga cac tgt cac cag cac aaa tac tgc 192
Leu Asp Thr Trp Asn Ala Glu Arg His Cys His Gln His Lys Tyr Cys
50 55 60

gac ccc aac cta ggg ctc cat gtc gag aag gag ggc acc tca gaa aca 240
Asp Pro Asn Leu Gly Leu His Val Glu Lys Glu Gly Thr Ser Glu Thr
65 70 75 80

gac acc act tgc acc tgc gat gaa ggt ctg cat tgt acc aac gct gcc 288
Asp Thr Thr Cys Thr Cys Asp Glu Gly Leu His Cys Thr Asn Ala Ala
85 90 95

tgt gag agc tgc acc atg cac agc ctg tgc ccc cct ggc ctg ggc gtc 336
Cys Glu Ser Cys Thr Met His Ser Leu Cys Pro Pro Gly Leu Gly Val
100 105 110

aaa cag atc gct aca ggg att tct gat acc atc tgc gat ccc tgc ccc 384
Lys Gln Ile Ala Thr Gly Ile Ser Asp Thr Ile Cys Asp Pro Cys Pro
115 120 125

atc ggc ttc ttc tcc aat gtg tct tct gct ttg gaa aag tgt cac cct 432
Ile Gly Phe Phe Ser Asn Val Ser Ser Ala Leu Glu Lys Cys His Pro
130 135 140

tgg acc agc tgt gaa acc aaa ggc ctg gtg aag gtt cag ggc gga act 480
Trp Thr Ser Cys Glu Thr Lys Gly Leu Val Lys Val Gln Ala Gly Thr
145 150 155 160

aac aag act gat gtt atc tgt ggt ccc cag cct cgg tta aga gcc ctg 528
Asn Lys Thr Asp Val Ile Cys Gly Pro Gln Pro Arg Leu Arg Ala Leu
165 170 175

gtg gtg gtc ccc atc att atg ggg atc ctg ctt gtt gtc ctg ttg gtg 576
Val Val Val Pro Ile Ile Met Gly Ile Leu Leu Val Val Leu Leu Val

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180	185	190	
tct gcc tgc atc cga aag gtg gtc aag aag cca gag aat aag gtt atc			624
Ser Ala Cys Ile Arg Lys Val Val Lys Lys Pro Glu Asn Lys Val Met			
195	200	205	
tat cag gac cct gtg gag gac ttg gag gaa ttt cct atg ccc ccg cac			672
Tyr Gln Asp Pro Val Glu Asp Leu Glu Glu Phe Pro Met Pro Pro His			
210	215	220	
tcc att gct ccg gtg caa gag acc tta cat ggg tgc cag ccc gtc acc			720
Ser Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln Pro Val Thr			
225	230	235	240
cag gag gac ggc aaa gag agc cgc atc tcc gtg cag gag aga gtg			765
Gln Glu Asp Gly Lys Glu Ser Arg Ile Ser Val Gln Glu Arg Val			
245	250	255	

<210> 58

<211> 255

<212> PRT

<213> Canis familiaris

<400> 58

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Gln Cys Cys Asn Met Cys Pro Pro Gly Glu Lys Leu Val Asn Asp Cys			
20	25	30	
Leu His Thr Ile Asp Thr Glu Cys Thr Arg Cys Gln Thr Gly Glu Phe			
35	40	45	
Leu Asp Thr Trp Asn Ala Glu Arg His Cys His Gln His Lys Tyr Cys			
50	55	60	
Asp Pro Asn Leu Gly Leu His Val Glu Lys Glu Gly Thr Ser Glu Thr			
65	70	75	80
Asp Thr Thr Cys Thr Cys Asp Glu Gly Leu His Cys Thr Asn Ala Ala			
85	90	95	
Cys Glu Ser Cys Thr Met His Ser Leu Cys Pro Pro Gly Leu Gly Val			
100	105	110	
Lys Gln Ile Ala Thr Gly Ile Ser Asp Thr Ile Cys Asp Pro Cys Pro			
115	120	125	

Ile Gly Phe Phe Ser Asn Val Ser Ser Ala Leu Glu Lys Cys His Pro
130 135 140

Trp Thr Ser Cys Glu Thr Lys Gly Leu Val Lys Val Gln Ala Gly Thr
145 150 155 160

Asn Lys Thr Asp Val Ile Cys Gly Pro Gln Pro Arg Leu Arg Ala Leu
165 170 175

Val Val Val Pro Ile Ile Met Gly Ile Leu Leu Val Val Leu Leu Val
180 185 190

Ser Ala Cys Ile Arg Lys Val Val Lys Lys Pro Glu Asn Lys Val Met
195 200 205

Tyr Gln Asp Pro Val Glu Asp Leu Glu Glu Phe Pro Met Pro Pro His
210 215 220

Ser Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln Pro Val Thr
225 230 235 240

Gln Glu Asp Gly Lys Glu Ser Arg Ile Ser Val Gln Glu Arg Val
245 250 255

<210> 59

<211> 769

<212> DNA

<213> Canis familiaris

<400> 59

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gtctccca ggttcctgat acataacctt attctctggc ttcttgacca cctttcggt 180

gcaggcagac accacagga caacaagcag gatcccata atgatgggga ccaccactag 240

ggctcttaac cgggctggg gaccacagat aacatcagtc ttgttagtgc ccgctgaa 300

cttcaccagg cctttgggtt cacagcttgt ccaagggtga cactttcca aagcagaaga 360

cacattggag agagagcga tggggcaggg atgcagatg gtatcagaa tccctgtago 420

gatctgttg actccagga cagggggga caggctgtgc atgggtgcagc tctcacagga 480

agcgttggtta caatgcagac cttcatcgca tgtgcaagtg gtgtctgttt ctgacgtgcc 540
 ctccctctcg acatggagcc ctagggtggg gtcgcagtat ttgtgctggg gacagtgtct 600
 ctctgcgttc caagtgtctt ggasttcgcc tgtttggcaa cgagtgcatt ccgtgtcaat 660
 ggtatgtagg cagtcattca ccagtttctc tctggtggg cacatattac agcactgact 720
 gtctactagg tattgctttt ctctgcacgc agtgcgtggg tctgg 765

<210> 60

<211> 336

<212> DNA

<213> *Felis catus*

<220>

<221> CDS

<222> {1}..(336)

<400> 60

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 Asn Val Ser Ser Ala Ser Glu Lys Cys His Pro Trp Thr Arg Cys Glu
 1 5 10 15

acc aaa ggc ctg gtg gag ctt cag gcg ggg acc aac aag acg gat gcc 96
 Thr Lys Gly Leu Val Glu Leu Gln Ala Gly Thr Asn Lys Thr Asp Ala
 20 25 30

gtc tgc ggt ttc cag gat cgg ata aga gcc ctg gtg gtg atc ccc atc 144
 Val Cys Gly Phe Gln Asp Arg Ile Arg Ala Leu Val Val Ile Pro Ile
 35 40 45

acg atg gtg gtc ctg ctt gct gtc ttg ttg gtg tct gcg tat atc aga 192
 Thr Met Val Val Leu Leu Ala Val Leu Leu Val Ser Ala Tyr Ile Arg
 50 55 60

aag gtg acc aag aag cca gag aat aag gtc ctg cag cct aag gct gtg 240
 Lys Val Thr Lys Lys Pro Glu Asn Lys Val Leu Gln Pro Lys Ala Val
 65 70 75 80

tcc cag gac cct gtg gag gac ttg gag gtc ctt cct gtc ccc ctg cac 288
 Ser Gln Asp Pro Val Glu Asp Leu Glu Val Leu Pro Val Pro Leu His
 85 90 95

ccc att gct ccg gtg cag gag acc tta caa ggg tgc cag ccg gtc acc 336
 Pro Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln Pro Val Thr
 100 105 110

<210> 61

<211> 112

<212> PRT

<213> Felis catus

<400> 61

Asn Val Ser Ser Ala Ser Glu Lys Cys His Pro Trp Thr Arg Cys Glu
1 5 10 15

Thr Lys Gly Leu Val Glu Leu Gln Ala Gly Thr Asn Lys Thr Asp Ala
20 25 30

Val Cys Gly Phe Gln Asp Arg Ile Arg Ala Leu Val Val Ile Pro Ile
35 40 45

Thr Met Val Val Leu Leu Ala Val Leu Leu Val Ser Ala Tyr Ile Arg
50 55 60

Lys Val Thr Lys Lys Pro Glu Asn Lys Val Leu Gln Pro Lys Ala Val
65 70 75 80

Ser Gln Asp Pro Val Glu Asp Leu Glu Val Leu Pro Val Pro Leu His
85 90 95

Pro Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln Pro Val Thr
100 105 110

<210> 62

<211> 336

<212> DNA

<213> Felis catus

<400> 62

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gaccaccatc gtgatgggga taccaccag ggtcttctc cgatcttga zaccgcagac 240
ggcatccgtc ttgttggtcc ccgctgag ctccaccagg cctttggtct caccctcgt 300
ccaggggtga cacttttccg aagcagatga cactt 336

<210> 63
 <211> 390
 <212> DNA
 <213> Canis familiaris

<400> 63
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 ggactctatt acgtctatgc ccaagtcacc ttctgctcca atcgggcagc ttcgagtcaa 180
 gctccgttcg tcgccagcct atgctccat tcccagtg gaacggagag agtcttactc 240
 cggcgccgca gctcccgagg ctgtccaaa ccttgcggcc aacagtcac cacttggga 300
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 gtgagccacg ggaccggctt cactctttt 390

<210> 64
 <211> 1878
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (284)..(1063)

<400> 64
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 gcgtcttaa ctactcctga gtaaggctgc cactttgaca gtgttttcat gctgcctctg 240
 ccaccttctc ggtctgaaga tatcatttca actctaacac agc atg atc gaa aca 295
 Met Ile Glu Thr
 1

tat agc caa act gct ccc cga tct gtg gcc act gga cca ccc gtc agt 343
 Tyr Ser Gln Thr Ala Pro Arg Ser Val Ala Thr Gly Pro Pro Val Ser
 5 10 15 20

atg aaa att ttt stg tat ttg ctt act gtt ttt ctc atc acc cag atg 391
 Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu Ile Thr Gln Met
 25 30 35

att gga tgg gca ctc ttt gct gta tat ctt cac aga aga ttg gac aag 439
 Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg Arg Leu Asp Lys
 40 45 50

ata gaa gat gaa agg aat ctt tat gaa gat ttt gtg ttc atg aaa acg 487
 Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe Met Lys Thr
 55 60 65

tta cag aaa tgc aac aaa ggg gag ggg tcc ttg tcc tta ctg aac tgt 535
 Leu Gln Lys Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu Leu Asn Cys
 70 75 80

gag gaa att aaa agc caa ttt gaa gcc ttt ctc aag gag ata atg cta 583
 Glu Glu Ile Lys Ser Gln Phe Glu Ala Phe Leu Lys Glu Ile Met Leu
 85 90 95 100

aac aac gaa atg aag aac gaa gaa aac att gca atg caa aaa ggt gat 631
 Asn Asn Glu Met Lys Lys Glu Glu Asn Ile Ala Met Gln Lys Gly Asp
 105 110 115

cag gat cct cga att gca gcc cat gtc ata agt gag gct agt agt aac 679
 Gln Asp Pro Arg Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Asn
 120 125 130

cca gcg tcc gtt ctg cgg tgg gcg cca aaa ggg tac tac acc ata agc 727
 Pro Ala Ser Val Leu Arg Trp Ala Pro Lys Gly Tyr Tyr Thr Ile Ser
 135 140 145

agc aac ctg gtg agc ctc gag aat ggg aaa cag ttg gcc gtg aaa aga 775
 Ser Asn Leu Val Ser Leu Glu Asn Gly Lys Gln Leu Ala Val Lys Arg
 150 155 160

caa gga ctc tat tac gtc tat gcc caa gtc acc ttc tgc tcc aat cgg 823
 Gln Gly Leu Tyr Tyr Val Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg
 165 170 175 180

gca gct tgg agt caa gct ccg ttc gtc gcc agc cta tgc ctc cat tcc 871
 Ala Ala Ser Ser Gln Ala Pro Phe Val Ala Ser Leu Cys Leu His Ser
 185 190 195

ccg agt gga acg gag aga gtc tta ctc cgc gcc gcg agc tcc cgc ggc 919
 Pro Ser Gly Thr Glu Arg Val Leu Leu Arg Ala Ala Ser Ser Arg Gly
 200 205 210

teg tcc aaa cct tgc ggc caa cag tcc atc cac ttg gga gga gta ttt 967
 Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe
 215 220 225

gaa ttg cat cca ggt gct tgc gtg ttc gtc aac gtg act gat cca agc 1015
 Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser
 230 235 240

caa gtg agc cac ggg acc ggc ttc acg tct ttt ggc tta ctc aaa ctc 1063
 Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu
 245 250 255 260

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<210> 65

<211> 260

<212> PRT

<213> Canis familiaris

<400> 65

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Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg	35	40	45
Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val	50	55	60
Phe Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ser Leu Ser	65	70	75
Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Ala Phe Leu Lys	85	90	95
Glu Ile Met Leu Asn Asn Glu Met Lys Lys Glu Glu Asn Ile Ala Met	100	105	110
Gln Lys Gly Asp Gln Asp Pro Arg Ile Ala Ala His Val Ile Ser Glu	115	120	125
Ala Ser Ser Asn Pro Ala Ser Val Leu Arg Trp Ala Pro Lys Gly Tyr	130	135	140
Tyr Thr Ile Ser Ser Asn Leu Val Ser Leu Glu Asn Gly Lys Gln Leu	145	150	155
Ala Val Lys Arg Gln Gly Leu Tyr Tyr Val Tyr Ala Gln Val Thr Phe	165	170	175
Cys Ser Asn Arg Ala Ala Ser Ser Gln Ala Pro Phe Val Ala Ser Leu	180	185	190
Cys Leu His Ser Pro Ser Gly Thr Glu Arg Val Leu Leu Arg Ala Ala	195	200	205
Ser Ser Arg Gly Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu	210	215	220
Gly Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val	225	230	235
Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly	245	250	255
Leu Leu Lys Leu			

<210> 66

<211> 1878

<212> DNA

<213> *Canis familiaris*

<400> 66

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 gtcttctctc ccagcaaaaa aagttacgta aaggtttttt tttttttttt tttttttttt 1800
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 tttcttcttc catcctt 1878

<210> 67

<211> 780

<212> DNA

<213> Canis familiaris

<400> 67

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 ctctttgctg tatatcttca cagaagattg gacaagatag aagatgaag gaatctttat 180
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 aacaacgaa tgaagaaag acaaacatt gcaatgcaaa aaggtgatca ggatcctcga 360
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 ccanaagggt actacaccat aagcagcaac ctggtgagcc tcgagaatgg gaacagttg 480

gccgtgaaa gacaaggact ctattacgtc tatgcccaag tcaccttctg ctccaatcgg 540
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tccatccact tgggaggagt atttgaattg catccaggtg ctccggtgtt cgtcaacgtg 720
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<210> 68

<211> 780

<212> DNA

<213> Canis familiaris

<400> 68

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ctgttggccg caaggttttg acgagccgcg ggagctccgc gcgcggagta agactctctc 180
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cgccacccgc agaacggacg ctgggttact actagcctca ctatgacat gggtgcgaat 420
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tagcattatc tccctgagaa aggttccaa ttggctttta atttctccac agttcaqtca 540
ggacaaggac cctccctt tgttgcaatt ctgtaacgtt ttcattgaca caaatcttc 600
ataaagattc ctttcatctt ctatcttgc caatcttctg tgaagatata cagcaagag 660
tgccgatcca atcatctggg tgatgagaa aacagtaagc anatacata aaattttcat 720
actgacgggt ggtccagtgg ccacagatcg gggagcagtt tggtctctg ttcgatcat 780

<210> 69

<211> 633

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> {1}..(633)

<400> 69

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ttg gac aag ata gaa gat gaa agg aat ctt tat gaa gat ttt gtg ttc      48
Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe
   1             5             10             15

atg aaa acc tta cag aac tgc aac aaa ggg gag ggg tcc ttg tcc tta      96
Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu
           20             25             30

ctg aac tgt gag gaa att aac agc caa ttt gaa gcc ttt ctc aag gag      144
Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Ala Phe Leu Lys Glu
           35             40             45

ata atg cta aac aac gaa atg aag aaa gaa gaa aac att gca atg caa      192
Ile Met Leu Asn Asn Glu Met Lys Lys Glu Glu Asn Ile Ala Met Gln
           50             55             60

aaa ggt gat cag gat cct cga att gca gcc cat gtc ata agt gag gct      240
Lys Gly Asp Gln Asp Pro Arg Ile Ala Ala His Val Ile Ser Glu Ala
           65             70             75             80

agt agt aac caa gcg tcc gtt ctg cgg tgg gcg cca aaa ggg tac tac      288
Ser Ser Asn Pro Ala Ser Val Leu Arg Trp Ala Pro Lys Gly Tyr Tyr
           85             90             95

acc ata agc agc aac ctg gtg agc ctc gag aat ggg aaa cag ttg gcc      336
Thr Ile Ser Ser Asn Leu Val Ser Leu Glu Asn Gly Lys Gln Leu Ala
           100            105            110

gtg aaa aga caa gga ctc tat tac gtc tat gcc caa gtc aac ttc tgc      384
Val Lys Arg Gln Gly Leu Tyr Tyr Val Tyr Ala Gln Val Thr Phe Cys
           115            120            125

tcc aat cgg gca gct tcg agt caa gct cgg ttc gtc gcc agc cta tgc      432
Ser Asn Arg Ala Ala Ser Ser Gln Ala Pro Phe Val Ala Ser Leu Cys
           130            135            140

ctc cat tcc ccg agt gga acg gag aga gtc tta ctc cgc gcc gcg agc      480
Leu His Ser Pro Ser Gly Thr Glu Arg Val Leu Leu Arg Ala Ala Ser
           145            150            155            160

tcc cgc gcc tcg tcc aac cct tgc ggc caa cag tcc atc cac ttg gga      528
Ser Arg Gly Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly

```

	165	170	175	
gga gta ttt gaa ttg cat cca ggt gct tcg gtg ttc gtc aac gtg act				576
Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr				
	180	185	190	
gat cca agc caa gtg agc cac ggg acc ggc ttc acg tct ttt ggc tta				624
Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu				
	195	200	205	
ctc aaa ctc				633
Leu Lys Leu				
	210			
<210> 70				
<211> 211				
<212> PRT				
<213> Canis familiaris				
<400> 70				
Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe				
1 5 10 15				
Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu				
20 25 30				
Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Ala Phe Leu Lys Glu				
35 40 45				
Ile Met Leu Asn Asn Glu Met Lys Lys Glu Glu Asn Ile Ala Met Gln				
50 55 60				
Lys Gly Asp Gln Asp Pro Arg Ile Ala Ala His Val Ile Ser Glu Ala				
65 70 75 80				
Ser Ser Asn Pro Ala Ser Val Leu Arg Trp Ala Pro Lys Gly Tyr Tyr				
85 90 95				
Thr Ile Ser Ser Asn Leu Val Ser Leu Glu Asn Gly Lys Gln Leu Ala				
100 105 110				
Val Lys Arg Gln Gly Leu Tyr Tyr Val Tyr Ala Gln Val Thr Phe Cys				
115 120 125				
Ser Asn Arg Ala Ala Ser Ser Gln Ala Pro Phe Val Ala Ser Leu Cys				
130 135 140				

Leu His Ser Pro Ser Gly Thr Glu Arg Val Leu Leu Arg Ala Ala Ser
 145 150 155 160

Ser Arg Gly Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly
 165 170 175

Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr
 180 185 190

Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu
 195 200 205

Leu Lys Leu
 210

<210> 71

<211> 633

<212> DNA

<213> Canis familiaris

<400> 71

gagtttgagt aagccaaag acgtgagcc ggtcccgtag ctcacttggc ttggatcagt 60
 cacgttgagc aacaccgaag cacttgatg cacttczaat actctccca agtggatgga 120
 ctgttgccg caaggtttgg acgagccgag ggaactcagc ggcggagta agactctctc 180
 cgttccactc ggggaatgga ggcataaggct ggcgaagaa ggaacttgac tcgaagctgc 240
 ccgattggag cagaaggatga ctggggcata gacgtaatag agtccttgc tttcacggc 300
 caactgtttc ccattctcga ggtccaccg gttgctgctt atggtgtagt acccttttgg 360
 cgcccacccg agaacggagc ctgggttact actagcctca ctctgacat gggctgcaat 420
 tcgaggatcc tgatcacctt ttgcatthc actgttttct tctttcttca ttctgtgtt 480
 tagcattrac tcttgagaa aggtttcaaa ttggctttta atttctcac agttcagtaa 540
 ggacaaggac ccttccccctt tgttgcatth ctgtaacgtt tctatgacaa caaatcttc 600
 ataaagattc ctttcatctt ctatcttgc caa 633

<210> 72

<211> 885

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (29)..(808)

<400> 72

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gaagataacca ttccaacttt aacacagc atg atc gaa aca tat agc caa act      52
                               Met Ile Glu Thr Tyr Ser Gln Thr
                               1                               5

gct ccc cgc tcc gtg gcc cct gga cca ccc gtc agt atg aaa att ttt      100
Ala Pro Arg Ser Val Ala Pro Gly Pro Pro Val Ser Met Lys Ile Phe
      10                               15                               20

atg tat tta ctt act ggg ttt ctc atc acc cag atg att ggg tca gca      148
Met Tyr Leu Leu Thr Val Phe Leu Ile Thr Gln Met Ile Gly Ser Ala
      25                               30                               35                               40

ctc ttt gct gtg tat ctt cac aga aga ctg gac aag ata gaa gat gaa      196
Leu Phe Ala Val Tyr Leu His Arg Arg Leu Asp Lys Ile Glu Asp Glu
                               45                               50                               55

agg aat ctt tat gaa gat ttt gtg ttc atg aaa aca tta cag aaa tgc      244
Arg Asn Leu Tyr Glu Asp Phe Val Phe Met Lys Thr Leu Gln Lys Cys
                               60                               65                               70

aac aaa gga gag ggg gcc tta tcc tta ctg aac tgt gag gaa att aaa      292
Asn Lys Gly Glu Gly Ala Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys
      75                               80                               85

agc cgg ttt gaa gcc ttt ctc aag gag ata atg cta aac aaa gaa acg      340
Ser Arg Phe Glu Ala Phe Leu Lys Glu Ile Met Leu Asn Lys Glu Thr
      90                               95                               100

aag aaa gaa aas aat gtt gca atg cas aaa ggc gac cag gat cct cga      388
Lys Lys Glu Lys Asn Val Ala Met Gln Lys Gly Asp Gln Asp Pro Arg
      105                               110                               115                               120

gtt gca gca cat gtc ata agt gag gcc agc agt agc aca gcg tct gtt      436
Val Ala Ala His Val Ile Ser Glu Ala Ser Ser Ser Thr Ala Ser Val
                               125                               130                               135

ctc cag tgg gcc ccc aaa ggc tac tac acc atc agc agc aac ttg gtg      484
Leu Gln Trp Ala Pro Lys Gly Tyr Tyr Thr Ile Ser Ser Asn Leu Val
      140                               145                               150

acc ctc gag aac ggg aag cag ctg gcc gtt aaa aga caa gga ctc tat      532

```

Thr Leu Glu Asn Gly Lys Gln Leu Ala Val Lys Arg Gln Gly Leu Tyr
 155 160 165
 tat atc tac gcc caa gtc acc ttc tgt tcc aat cgg gaa gct tgg agt 580
 Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser
 170 175 180
 caa gct cgg ttc ata gcc agc ctc tgc ctg cat tcc ccg agt gga tcc 628
 Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu His Ser Pro Ser Gly Ser
 185 190 195 200
 gag aga gtc tta ctc aga gct gca aat gcc cgc agt tcc tcc aaa ccc 676
 Glu Arg Val Leu Leu Arg Ala Ala Asn Ala Arg Ser Ser Ser Lys Pro
 205 210 215
 tgt ggg cag caa tcc att cac ttg gga gga gtc ttc gaa ctg cat cca 724
 Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu His Pro
 220 225 230
 ggt gct tgg gtg ttc gtg aac gtg act gat ccg agc caa gtg agc cac 772
 Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His
 235 240 245
 ggg acg ggc ttc acg tct ttt ggc ttg ctc aaa ctc tggacactgg 818
 Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu
 250 255 260
 cacctcgacg gccgcgagggc ctgcaggccg cggctgagct cacgctggga gtcttcacaa 878
 taccgca 885

<210> 73
 <211> 260
 <212> PRT
 <213> Felis catus

<400> 73
 Met Ile Glu Thr Tyr Ser Gln Thr Ala Pro Arg Ser Val Ala Pro Gly
 1 5 10 15
 Pro Pro Val Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
 20 25 30
 Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg
 35 40 45
 Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val

50	55	60
Phe Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ala Leu Ser		
65	70	75 80
Leu Leu Asn Cys Glu Glu Ile Lys Ser Arg Phe Glu Ala Phe Leu Lys		
85	90	95
Glu Ile Met Leu Asn Lys Glu Thr Lys Lys Glu Lys Asn Val Ala Met		
100	105	110
Gln Lys Gly Asp Gln Asp Pro Arg Val Ala Ala His Val Ile Ser Glu		
115	120	125
Ala Ser Ser Ser Thr Ala Ser Val Leu Gln Trp Ala Pro Lys Gly Tyr		
130	135	140
Tyr Thr Ile Ser Ser Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu		
145	150	155 160
Ala Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe		
165	170	175
Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu		
180	185	190
Cys Leu His Ser Pro Ser Gly Ser Glu Arg Val Leu Leu Arg Ala Ala		
195	200	205
Asn Ala Arg Ser Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu		
210	215	220
Gly Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val		
225	230	235 240
Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly		
245	250	255
Leu Leu Lys Leu		
260		

<210> 74

<211> B85

<212> DNA

<213> Felis catus

<400> 74

tgcgtatta tgaagactcc cagcgtgagc tcagccgcgc cctgcagccc tcgcggcctg 60
 cgaggcgcca gtcgttcagag tttagcgaag ccaaaagacg tgaagcccgt cccgtgctc 120
 acttggtctg gatcagtcac gttcacgaac accgaagcac ctggatgcag ttcgaagact 180
 cctcccaagt gaatggattg ctgccacag ggtttggagg aactgcgggc attgcagct 240
 ctgagtaaga ctctctcgga tccactcggg gaatgcaggc agsggctggc tatgaacgga 300
 gcttgactcg aagcttcccg attggaacag aaggtagctt gggcgtagat ataataagat 360
 ccttgctttt taccggccag ctgottcccg ttctcgaggg tcaccaagtt gctgcttatg 420
 gctgtagtgc ctttgggggc ccaactggaga acagacgctg tgcctactgt ggctcactt 480
 atgacatgtg ctgcaactcg aggatcctgg tcgccttttt gcattgcac attttttct 540
 ttcttcgttt ctttgtttag cattatctcc ttgagaaagg ctccaacccg gcttttaatt 600
 tctcacagt tcagtaagga tsaggccccc tctccttctg tgcatttctg taatgtttc 660
 atgaacacaa aatcttcata aagattcctt tcatcttcta tcttgctcag tcttctgtga 720
 agtacacag caaagagtgc tgaccaatc atctgggtga tgagaaacac agtaagttaa 780
 tacstaasaa ttttcatact gacgggtggc ccaggggcca cggagcgggg agcagtttgg 840
 ctatatgttt cgatcatgct gtgttaaggt tgaatggta tcttc 885

<210> 75

<211> 780

<212> DNA

<213> Felis catus

<400> 75

atgategaaa catatagcca aactgctccc cgctccgtgg cccctggacc accgttcagt 60
 atgaaaattt ttatgtattt acttaactgtg ttctcatca cccagatgat tgggtcagca 120
 ctctttgctg tgtctcttca cagaagactg gacagagtag aagatgaaag gcatctttat 180
 gaagattttg tgttcattga accattacag aaatgcacaa aaggagaggg ggcttatcc 240
 ttactgaact gtgaggaaat taagagcccg tttagagcct ttctcaaggc gataatgcta 300
 aacaaagaaa cgaagaaaga aaaaaatgtt gcaatgcasa aaggcgacca gcatcctcga 360

gttgacgac atgtcataag tgaggccagc agtagcacag cgtctgttct ccagtgggcc 420
 cccsaaggct actacaccat aagcagcaac ttggtgaccc tcgagaacgg gaagcagctg 480
 gccgttaaaa gacaaggact ctattatata tscgccaaag tcacottctg tccaatcgg 540
 gaagcttcga gtcaggctcc gtccatagcc agcctctgac tgcattcccc gagtggatcc 600
 gagagagtct tactcagagc tgcgaatgcc cgcagttcct ccaaacctg tgggcagcag 660
 tccattcact tgggaggagt ctccgaactg cctccagggt ctccgggtgt cgtgaacgtg 720
 actgatccga gccaaagtga ccacgggacg ggcttcacgt cttttggctt gctcaaacct 780

<210> 76

<211> 780

<212> DNA

<213> Felis catus

<400> 76

gagtttgagc aagccaaaag acgtgaagcc cgtcccgtgg ctcccttggc tcggatcagt 60
 caagtccagc aacaccgagc caactggatg cagttcgagc actccctcca agtgaatgga 120
 ttgctgccc aagggttttg aggaactgag ggcatttgca gctctgagta agactctctc 180
 ggatccactc ggggaatgca ggcagaggct ggctatgaac ggagcttgac tcgaagcttc 240
 ccgattggaa cagaaggtga ctggggcgta gatataatag agtcccttgc ttttascggc 300
 cagctgcttc ccgttctcga gggtcaccaa gtgctgctt atgggtgtagt agcctttggg 360
 ggcccactgg agaacagacg ctgtgctact gctggcctca cttatgacat gtgctgcaac 420
 tcgaggatcc tggctgcctt tttgcattgc aacatttttt tctttcttcg tttctttgtt 480
 tagcattatc tctttgagaa aggttcacaa ccggcttita atttctcac agttcagtas 540
 ggataaggcc cctctctctt tgttgcattt ctgtaatgtt ttcattgaaa caaatcttc 600
 ataaagattc cttctctctt ctatcttgc cagctctctg tgaagataca cagcaazgag 660
 tgcagaccca atcatctggg tgatgagaaa cacagtazgt aattacataa aattttctat 720
 actgacgggt ggtccagggg ccacgggagc gggagcagtt tggctatctg tttcgatcat 780

<210> 77
 <211> 633
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(633)

<400> 77

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ctg gac aag ata gaa gat gaa agg aat ctt tat gaa gat ttt gtg ttc      48
Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe
   1             5             10             15

atg aaa aca tta cag aaa tgc aac aaa gga gag ggg gcc tta tcc tta      96
Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ala Leu Ser Leu
           20             25             30

ctg aac tgt gag gaa att aag agc cgg ttt gaa gcc ttt ctc aag gag      144
Leu Asn Cys Glu Glu Ile Lys Ser Arg Phe Glu Ala Phe Leu Lys Glu
           35             40             45

ata atg cta aac aaa gag aag aag aaa gaa aaa aat gtt gca atg caa      192
Ile Met Leu Asn Lys Glu Thr Lys Lys Glu Lys Asn Val Ala Met Glu
           50             55             60

aaa ggc gac cag gat cct cga gtt gca gca cat gtc ata agt gag gcc      240
Lys Gly Asp Gln Asp Pro Arg Val Ala Ala His Val Ile Ser Glu Ala
           65             70             75             80

agc agt age aca gag tct gtt ctc cag tgg gcc ccc aag ggc tac tac      288
Ser Ser Ser Thr Ala Ser Val Leu Gln Trp Ala Pro Lys Gly Tyr Tyr
           85             90             95

acc ata agc age aac ttg gtg acc ctc gag aac ggg aag cag ctg gcc      336
Thr Ile Ser Ser Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Ala
           100            105            110

gtt aaa aga cca gga ctc tat tat atc tac gcc caa gtc acc ttc tgt      384
Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys
           115            120            125

tcc aat cgg gaa gct tog agt caa gct ccg ttc ata gcc agc ctc tgc      432
Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys
           130            135            140

ctg cat tcc ccg agt gga tcc gag aga gtc tta ctc aga gct gca aat      480

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Leu His Ser Pro Ser Gly Ser Glu Arg Val Leu Leu Arg Ala Ala Asn
 145 150 155 160

gcc cgc agt tcc tcc aaa ccc tgt ggg cag caa tcc att cac ttg gga 528
 Ala Arg Ser Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly
 165 170 175

ggg gtc ttc gaa ctg cat cca ggt gct tcg gtg ttc gtg aac gtg act 576
 Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr
 180 185 190

gat ccg agc caa gtg agc cac ggg acg ggc ttc acg tct ttt ggc ttg 624
 Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu
 195 200 205

ctc aac ctc 633
 Leu Lys Leu
 210

<210> 78

<211> 211

<212> FRT

<213> Felis catus

<400> 78

Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe
 1 5 10 15

Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ala Leu Ser Leu
 20 25 30

Leu Asn Cys Glu Glu Ile Lys Ser Arg Phe Glu Ala Phe Leu Lys Glu
 35 40 45

Ile Met Leu Asn Lys Glu Thr Lys Lys Glu Lys Asn Val Ala Met Gln
 50 55 60

Lys Gly Asp Gln Asp Pro Arg Val Ala Ala His Val Ile Ser Glu Ala
 65 70 75 80

Ser Ser Ser Thr Ala Ser Val Leu Gln Trp Ala Pro Lys Gly Tyr Tyr
 85 90 95

Thr Ile Ser Ser Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Ala
 100 105 110

Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys

115	120	125
Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys		
130	135	140
Leu His Ser Pro Ser Gly Ser Glu Arg Val Leu Leu Arg Ala Ala Asn		
145	150	155 160
Ala Arg Ser Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly		
	165	170 175
Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr		
	180	185 190
Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu		
	195	200 205
Leu Lys Leu		
210		

<210> 79

<211> 633

<212> DNA

<213> Felis catus

<400> 79

gagtttgagc aagcccaaaag acgtgaagcc cgtcccgtagg ctcacttggc tggatcagt 60
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 ttgctgccc aagggtttgg aggaactgag ggcatttgca gctctgagta agactctctc 180
 ggatccactc ggggaatgca ggcagaggct ggctatgaac ggagcttgac tcgaagcttc 240
 ccgattggaa cagaagggtga cttggggcga gatataatag agtccttgtc ttttaacggc 300
 cagctgcttc ccgttctcga gggtcaccaa gttgctgctt atgggtgtagt agcctttggg 360
 ggcccactgg agaacagacg ctgtgctact gctggcctca cttatgacat gtgctgcaac 420
 tcggggatcc tggtcgcctt tttgcattgc aacatttttt tctttctctg tttctttggt 480
 tagcattatc tccttgagaa aggttcaca caggctttta atttctcacc agttcagtaa 540
 ggataaggcc cctctctctt tgttgcaatt ctgtaatggt ttcattgaca caaatcttc 600
 ataaagattc ctttcatctt ctatcttgtc cag 633

<210> 80

<211> 610

<212> DNA

<213> *Canis familiaris*

<220>

<221> CDS

<222> (29) .. (430)

<400> 80

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caaggcaaac actgaacatt tcagagct atg aga atg ctt ctg aat ttg agt      52
                               Met Arg Met Leu Leu Asn Leu Ser
                               1                               5

ttg cta gct ctt ggg gct gcc tat gtt tct gcc ttt gct gta gaa aat      100
Leu Leu Ala Leu Gly Ala Ala Tyr Val Ser Ala Phe Ala Val Glu Asn
    10                               15                               20

ccc atg aat aga ctg gtg gca gag acc ttg aca ctg ctc tcc act cat      148
Pro Met Asn Arg Leu Val Ala Glu Thr Leu Thr Leu Leu Ser Thr His
    25                               30                               35                               40

cga act tgg ctg ata ggc gat ggg aac ctg atg att cct act cct gaa      196
Arg Thr Trp Leu Ile Gly Asp Gly Asn Leu Met Ile Pro Thr Pro Glu
                               45                               50                               55

aat aaa aat cac caa ctg tgc att aaa gaa gtt ttt cag ggt ata gac      244
Asn Lys Asn His Gln Leu Cys Ile Lys Glu Val Phe Gln Gly Ile Asp
                               60                               65                               70

aca ttg aag aac caa act gcc cac ggg gag gct gtg gat aaa cta ttc      292
Thr Leu Lys Asn Gln Thr Ala His Gly Glu Ala Val Asp Lys Leu Phe
    75                               80                               85

caa aac ttg tct tta ata aaa gaa cac ata gag cgc cca aaa aaa agg      340
Gln Asn Leu Ser Leu Ile Lys Glu His Ile Glu Arg Gln Lys Lys Arg
    90                               95                               100

tgt gca gga gaa aga tgg aga gtg aca aag ttc cta gac tac ctg caa      388
Cys Ala Gly Glu Arg Trp Arg Val Thr Lys Phe Leu Asp Tyr Leu Gln
    105                               110                               115                               120

gta ttt ctt ggt gta ata aac acc gag tgg aca ccg gaa agt      430
Val Phe Leu Gly Val Ile Asn Thr Glu Trp Thr Pro Glu Ser
    125                               130

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tgagaccaa ccggttatt gtatgggaag attttggaga agaattggtt ttggcgatg 490
 agaatgaggg ccaaccaaca gtatgggactt aatggccagt ataactaagg ttcagagaca 550
 aagttaatat ttcaggcatc ctactacttt atcacttcac acagatgaaa tatatttgag 610

<210> 81

<211> 134

<212> PRT

<213> Canis familiaris

<400> 81

Met Arg Met Leu Leu Asn Leu Ser Leu Leu Ala Leu Gly Ala Ala Tyr
 1 5 10 15

Val Ser Ala Phe Ala Val Glu Asn Pro Met Asn Arg Leu Val Ala Glu
 20 25 30

Thr Leu Thr Leu Leu Ser Thr His Arg Thr Trp Leu Ile Gly Asp Gly
 35 40 45

Asn Leu Met Ile Pro Thr Pro Glu Asn Lys Asn His Gln Leu Cys Ile
 50 55 60

Lys Glu Val Phe Gln Gly Ile Asp Thr Leu Lys Asn Gln Thr Ala His
 65 70 75 80

Gly Glu Ala Val Asp Lys Leu Phe Gln Asn Leu Ser Leu Ile Lys Glu
 85 90 95

His Ile Glu Arg Gln Lys Lys Arg Cys Ala Gly Glu Arg Trp Arg Val
 100 105 110

Thr Lys Phe Leu Asp Tyr Leu Gln Val Phe Leu Gly Val Ile Asn Thr
 115 120 125

Glu Trp Thr Pro Glu Ser
 130

<210> 82

<211> 610

<212> DNA

<213> Canis familiaris

<400> 82

ctcaastata ttcatctgt gtgaagtgat aagtagtag gatgcctgaa atatttactt 60

tgtctctgaa gcttagttat actggccatt aagtcctac tgttggttgg cctctattct 120
 catcgccaaa aaaccattct tctccaaat ctccactac aataagccgg ttgttctca 180
 actttccggt gtcactcgg tgtttattac accagaaat acttgcagg agtctaggaa 240
 cttgtcact ctccattctt ctctgcaca ctttttttt tggcgtcta tgtgttctt 300
 tattaagac aagttttgga atagtttct cacagctcc cgtgggcag ttgtttctt 360
 caatgtgtct atacctgaa aaacttctt aatgcacagt tggtagttt tattttcagg 420
 agtaggaatc atcaggttcc catcgctat cagccagtt cgtgagtgg agagcagtgt 480
 caaggtctct gccaccagtc tattctggg attttctac gcaaggcag aaacataggc 540
 agccccaaga gctagcaaac tcaattcag aagcattct atagctctga aatgttcagt 600
 gtttgccctg 610

<210> B3
 <211> 402
 <212> DNA
 <213> Canis familiaris

<400> B3
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 gctgtagaaa atcccatgaa tagactggtg gcagagacct tgacactgt ctccactcat 120
 cgaacttggc tgataggcga tgggaacctg atgattcta ctctgaaaa taaaaatcac 180
 caactgtgca ttaagagagt ttttcagggt atagacacat tgaagaacca aactgcccac 240
 ggggaggctg tggataaact attccaaaac ttgtctttta taaagaaca catagagcgc 300
 caaaaaaaaaa ggtgtgcagg agaaagatgg agagtgaaca agttctaga ctacctgca 360
 gtatttcttg gtgtaataaa caccagtggt acaccggaaa gt 402

<210> B4
 <211> 402
 <212> DNA
 <213> Canis familiaris

<400> 84

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ctttgtcact ctccatcttt ctccctgcaca cttttttttt tggcgcctta tgtgttcttt 120
tattaaagac aagttttgga atagtattac cacagcctcc ccgtgggcag tttggttctt 180
caatgtgtct staccctgaa aaactttctt aatgcacagt tgggtgatttt tattttcagg 240
agttaggaatc atcaggttcc cctgccttat cagccaagtt cgatgagtg agagcagtg 300
caaggtctct gccaccagtc tattcatggg attttctaca gcaaaggcag aacatagga 360
agccccaaga gctagcaaac tcaaatcag agcattctc at 402

<210> 85

<211> 345

<212> DNA

<213> *Canis familiaris*

<220>

<221> CDS

<222> (1)..(345)

<400> 85

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Phe Ala Val Glu Asn Pro Met Asn Arg Leu Val Ala Glu Thr Leu Thr	
1 5 10 15	
ctg ctg tcc act cat cga act tgg ctg ata ggc gat ggg aac ctg atg	96
Leu Leu Ser Thr His Arg Thr Trp Leu Ile Gly Asp Gly Asn Leu Met	
20 25 30	
att cct act cct gaa aat aaa aat cac caa ctg tgc att aaa gaa gtt	144
Ile Pro Thr Pro Glu Asn Lys Asn His Gln Leu Cys Ile Lys Glu Val	
35 40 45	
ttt cag ggt ata gac aca ttg aag aac caa act gcc cac ggg gag gct	192
Phe Gln Gly Ile Asp Thr Leu Lys Asn Gln Thr Ala His Gly Glu Ala	
50 55 60	
gtg gat aaa cta ttc caa aac ttg tct tta ata aaa gaa cac ata gag	240
Val Asp Lys Leu Phe Gln Asn Leu Ser Leu Ile Lys Glu His Ile Glu	
65 70 75 80	
cgc caa aaa aaa agg tgt gca gga gaa aga tgg aga gtg aca aag ttc	288
Arg Gln Lys Lys Arg Cys Ala Gly Glu Arg Trp Arg Val Thr Lys Phe	

	85	90	95	
cta gac tac ctg cca gta ttt ctt ggc gta ata aac acc gag tgg aca				336
Leu Asp Tyr Leu Gln Val Phe Leu Gly Val Ile Asn Thr Glu Trp Thr				
	100	105	110	

ccg gaa agt				345
Pro Glu Ser				
	115			

<210> 86
 <211> 115
 <212> PRT
 <213> Canis familiaris

<400> 86				
Phe Ala Val Glu Asn Pro Met Asn Arg Leu Val Ala Glu Thr Leu Thr				
1	5	10	15	

Leu Leu Ser Thr His Arg Thr Trp Leu Ile Gly Asp Gly Asn Leu Met				
20	25	30		

Ile Pro Thr Pro Glu Asn Lys Asn His Gln Leu Cys Ile Lys Glu Val				
35	40	45		

Phe Gln Gly Ile Asp Thr Leu Lys Asn Gln Thr Ala His Gly Glu Ala				
50	55	60		

Val Asp Lys Leu Phe Gln Asn Leu Ser Leu Ile Lys Glu His Ile Glu				
65	70	75	80	

Arg Gln Lys Lys Arg Cys Ala Gly Glu Arg Trp Arg Val Thr Lys Phe				
85	90	95		

Leu Asp Tyr Leu Gln Val Phe Leu Gly Val Ile Asn Thr Glu Trp Thr				
100	105	110		

Pro Glu Ser	
115	

<210> 87
 <211> 345
 <212> DNA
 <213> Canis familiaris

<400> 87

actttccggt gtccactogg tgtttattac accaagaat acttgcagggt agtctaggaa 60
 ctttgtcact ctccatcttt ctctgcaca ctttttttt ttggcctcta tgtgttcttt 120
 tattaaagac aagttttgga atagtttate cacagcctcc ccgtgggcag ttgggttctt 180
 caatgtgtct atccctgaa aaacttcttt atgcacagt tgggtatttt tattttcagg 240
 agtaggaatc atcaggttcc cctgcctat cagccaagt cgatgagtgg agagcagtgt 300
 caaggctctt gccaccagtc tattcatggg attttctaca gcaaa 345

<210> 88

<211> 166

<212> DNA

<213> Canis familiaris

<400> 88

ctacgttag gccagcctac gacctgcctg ctcttccctc gctcctcctg cattggctct 60
 gggctccatg ggcctctggt tgactgtggt cattgctctc acctgcctcg gtggccttgc 120
 ctcccagagc cctgtgactc cctcccccac cctcaaggag ctcat 166

<210> 89

<211> 272

<212> DNA

<213> Canis familiaris

<400> 89

tggccttgcc tcccagagcc ctgtgactcc ctcccacc ctcaggagc tcattgagga 60
 gctggtcaac atcaaccaga atcaggctc cctctgcaac ggcagcatgg tgtggagcgt 120
 caacctgacc gccggcatgt actgcgcage tctagaatct ctggtcaatg tctccgactg 180
 cagcgcctc caaaggaccc agaggatgt gasagcactg tgcctccaa agcccgcggc 240
 agggcagatt tccagtgaac gcagccgaga ca 272

<210> 90

<211> 278

<212> DNA

<213> Canis familiaris

<400> 90

atggcgctct ggttgactgt ggtcattggt ctcacctgcc tcggtggcct tgcctccccg 60
agccctgtga ctccctcccc aacctcaag gagctcattg aggagctggt caacataacc 120
cagaatcagg catccctctg caacggcagc atggtgtgga gctcaacct gaccgcccgc 180
atgtactgag cagctctaga atctctgata aatgtctccg actgcagcgc catccaaagg 240
accagagga tgcctgaaagc actgtgctct caaaagcc 278

<210> 91

<211> 1302

<212> DNA

<213> *Canis familiaris*

<220>

<221> CDS

<222> [52]..(444)

<400> 91

ctacgacctg cctgctcttc cctcgtctct cctgcattgg ctctgggctc c atg gcc 57
Met Ala
1

ctc tgg ttg act gtg gtc att gct ctc acc tgc ctc ggt ggc ctt gcc 105
Leu Trp Leu Thr Val Val Ile Ala Leu Thr Cys Leu Gly Gly Leu Ala
5 10 15

tcg ccg agc cct gtg act ccc tcc cca acc ctc aag gag ctc att gag 153
Ser Pro Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu
20 25 30

gag ctg gtc aac atc acc cag aat cag gca tcc ctc tgc aac ggc agc 201
Glu Leu Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser
35 40 45 50

atg gtg tgg agc gtc aac ctg acc gcc ggc atg tac tgc gca gct cta 249
Met Val Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu
55 60 65

gaa tcc ctg atc aat gtc tcc gac tgc agc gcc atc caa agg acc cag 297
Glu Ser Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln
70 75 80

agg atg ctg aaa gca ctg tgc tct caa aag ccc ggc gca ggg cag att 345
Arg Met Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Gln Ile

85

90

95

tcc agt gaa cgc agc cga gac acc aaa att gaa gtg atc cag ttg gtg 393
 Ser Ser Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val
 100 105 110

aaa aac ctg ctc acc tat gta agg gga gtt tat cgc cat gga aat ttc 441
 Lys Asn Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe
 115 120 125 130

aga tgaagcatga aaacttagca tccattatctg tagaccacga cctgaccact 494
 Arg

taagtccag atccattttt ctctccgacg tcacaaattt cttagggagg tggggggggg 554

ggagaaccat ttcttcagct gggacctcag cctgcacccg ctgcctccat ggagctgagc 614

ccagccacc ctgccttggt gcctggggcc cagcgggtg gccctccctc gtctgcactt 674

catcaacgct gagggaaagc actgcaccc atgactgtcc cctctcaga gcaagtgca 734

gcattacagt ggaggcagat atgtgtggga ggggtcttg ctgtacctgg gaggggcacc 794

gacatgttc ttcttagcct tatttattat tgtgtgttat ttaacaagt gctttgttt 854

gtgttggga caggagtggt cttagagctg ggggccaggt gactgggtt tagagagtc 914

ctgggaetac gcactgtgtg taaaattctg ctacctact gggatcctgg ggcagacaca 974

ggggacagga gaaagggtca gagatgctgc tcttgtctgc cactcagcag ctggccctca 1034

gccagcaggt aatttattgt ttctccttgt atttaaggt aagaaacaaa atatgttctc 1094

aaagagttaa taatatatag aagagtagcc taaaaggctg ctttgggtgt gtgtggccag 1154

gccggggcgg gtggggggga ggtgtgtgtc actgaatgtg ctctttcact gactttgtca 1214

aactggaagc cagaaataaa gatggtgaca agagaacaaa aaaaacaaa aaaaacaaa 1274

aaaaacaaa aaaaacaaa aaaaacaaa 1302

<210> 92

<211> 131

<212> PRT

<213> Canis familiaris

<400> 92

Met Ala Leu Trp Leu Thr Val Val Ile Ala Leu Thr Cys Leu Gly Gly
 1 5 10 15

Leu Ala Ser Pro Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu
 20 25 30

Ile Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn
 35 40 45

Gly Ser Met Val Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala
 50 55 60

Ala Leu Glu Ser Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg
 65 70 75 80

Thr Gln Arg Met Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly
 85 90 95

Gln Ile Ser Ser Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln
 100 105 110

Leu Val Lys Asn Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly
 115 120 125

Asn Phe Arg
 130

<210> 93

<211> 1302

<212> DNA

<213> Canis familiaris

<400> 93

tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60

tcaccatctt tttttctggc ttccagtttg acaaagtcag tgaaagagca cattcagtga 120

caacaccctc cccccccccc gcccgggctt ggccacacac acccaatgca gcccttttagg 180

ctactctctt ctatattatt acctctttga taacatattt tttttcttaa cttaaatatc 240

aaggaaaac aataaatatc tgcttggctg agggccagct gctgagtggc agacaagagc 300

agcatctctg accctttctc ctgtcccttg tctcgccccc aggstcccg tgaggttagca 360

gaattttaca cacagtgcct attcccaggg actctctaaa cccgagtcac tgggccccca 420

gctccaagcc actccctgtc cccagcacaa acaagacac ttgtttaaat aacacacaa 480
 aataaataag gctaagaaga aacatgtctg tgccactccc aggtacagca agacccctc 540
 ccacacatat ctgcctccac tgtaatgtg cactttgctc tgaggagggg acagtcctgg 600
 gatgcagtcg ttccctcag cgttgatgaa gtgcagacgg aggagggcca cccggctggg 660
 ccccatgcac caaggcaggg gtggctgggc tcagctccat gggaggcagg ggtgcaggct 720
 gaggtcccag ctgaggaaat ggttctccc cccccacc tccctagaa atttgtgacg 780
 tcggaangaa aaatgcatct ggaacttaag tggtcaggtc tgggtctaca gataaggatg 840
 ctaagtttct atgcttctc tgaatttcc atggcgataa actccctta catagggtgag 900
 caggttttct accaactgga tcaattcaat ttgtgtgtct cggctgcgtt cactggaaat 960
 ctgcctgccc gggggtttt gagagcacag tgctttcagc atctctggg tcccttgat 1020
 ggcgctgcag tcggagacat tgatcagagc ttctagagct ggcagctaca tgccggcggc 1080
 caggttgacg ctccacacca tgcctccgtt gcagggggat gctgattct ggggtgatgt 1140
 gaccagctcc tcaatgagct ccttgagggt tggggaggga gtacagggc tcggggaggc 1200
 aaggccaccg aggcaggtga gagcaatgac cacagtcaac cagagcgcca tggagcccag 1260
 agccaatgca ggaggagcga gggagagca ggcaggtcgt ag 1302

<210> 94

<211> 393

<212> DNA

<213> Canis familiaris

<400> 94

atggcgctct ggttgactgt ggtcattgct ctacctgccc tgggtggcct tgctccccc 60
 agccctgtga ctccctccc aacctcaag gagctcattg aggagctggt caacatcacc 120
 cagaatcagg catccctctg caacggcagg atggtgtgga ggtcaacct gaccgcgggc 180
 atgtactgcs cagctctaga atctctgato aatgtctccg actgcagcgc catccsaagg 240
 acccagagga tgctgaaagc actgtgtctct caaaagcccg cggcagggca gatttccagt 300
 gaacgcagcc gagacaccaa aattgagtg atccagtttg tggaaacct gctcaacct 360

gtasggggag tttatcgcca tggaaatttc aga

393

<210> 95

<211> 393

<212> DNA

<213> Canis familiaris

<400> 95

tetgaattt ccattggcat aaactccctt tacataggtg agcaggtttt tcaccaactg 60
gatacttca attttgggtg ctgggttgcg ttcaactgga atctgacctg ccgggggctt 120
ttgagagcac agtgccttca gcattcctctg ggtccttttg atggcgctgc agtcggagac 180
attgatcaga gattctagag ctggcgagta catgccggcg gtcaggttga cgtccacac 240
catgctgccc ttgcagaggg atgctgatt ctgggtgatg ttgaccagct cctcaatgag 300
ctccttgagg gttggggagg gattcacagg gctcggggag gcsaggccac ccaggcaggc 360
gagagcaatg accacagtca accagagcgc cat 393

<210> 96

<211> 333

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(333)

<400> 96

agc	cct	gtg	act	ccc	tcc	cca	acc	ctc	aag	gag	ctc	att	gag	gag	ctg	48
Ser	Pro	Val	Thr	Pro	Ser	Pro	Thr	Leu	Lys	Glu	Leu	Ile	Glu	Glu	Leu	
1				5					10					15		
gtc	aac	atc	acc	cag	aat	cag	gca	tcc	ctc	tgc	aac	ggc	agc	atg	gtg	96
Val	Asn	Ile	Thr	Gln	Asn	Gln	Ala	Ser	Leu	Cys	Asn	Gly	Ser	Met	Val	
			20					25					30			
tgg	agc	gtc	aac	ctg	acc	gcc	ggc	atg	tac	tgc	gca	gct	ctc	gaa	tct	144
Trp	Ser	Val	Asn	Leu	Thr	Ala	Gly	Met	Tyr	Cys	Ala	Ala	Leu	Glu	Ser	
			35				40					45				
ctg	atc	aat	gtc	tcc	gac	tgc	agc	gcc	atc	caa	agg	acc	cag	agg	atg	192

Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln Arg Met
 50 55 60

ctg aaa gca ctg tgc tct caa aag ccc gcg gca ggg cag att tcc agt 240
 Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Gln Ile Ser Ser
 65 70 75 80

gaa cgc agc cga gac acc aaa att gaa gtg atc cag ttg gtg aaa aac 288
 Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val Lys Asn
 85 90 95

ctg ctc acc tat gta agg gga gtt tat cgc cat gga aat ttc aga 333
 Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe Arg
 100 105 110

<210> 97

<211> 111

<212> PRT

<213> Canis familiaris

<400> 97

Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu Glu Leu
 1 5 10 15

Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser Met Val
 20 25 30

Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser
 35 40 45

Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln Arg Met
 50 55 60

Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Gln Ile Ser Ser
 65 70 75 80

Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val Lys Asn
 85 90 95

Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe Arg
 100 105 110

<210> 98

<211> 333

<212> DNA

<213> Canis familiaris

<400> 98

tctgaaattt ccattgggat aaactccctt tacataggtg agcaggcttt taccnaactg 60
 gacacattca attttggtgt ctgggtgctg ttcactggaa atctgacctg ccgagggttt 120
 ttgagagcac agtgcattca gcatactctg ggtccttttg atggcgctgc agtcggagac 180
 attgacaga gattctagag ctgcgcagta catgccggcg gtcaggttga cgtccscac 240
 catgctgccg ttgcagaggg atgcttgatt ctgggtgctg ttgaccagct cctcaatgag 300
 cctcttgagg gttggggagg gagtcacagg gct 333

<210> 99

<211> 1269

<212> DNA

<213> *Canis familiaris*

<220>

<221> CDS

<222> (57)...[446]

<400> 99

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 Met
 1

gcg ctc tgg ttg act gtg gtc att gct ctc acc tgc ctc ggt ggc ctt 107
 Ala Leu Trp Leu Thr Val Val Ile Ala Leu Thr Cys Leu Gly Gly Leu
 5 10 15

gcc tcc ccg agc cct gtg act ccc tcc cca acc ctc aag gag ctc att 155
 Ala Ser Pro Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile
 20 25 30

gag gag ctg gtc aac atc acc cag aat ccg gca tcc ctc tgc aac ggc 203
 Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly
 35 40 45

agc atg gtg tgg agc gtc aac ctg acc gcc ggc atg tac tgc gca gct 251
 Ser Met Val Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
 50 55 60 65

cta gaa tct ctg atc aat gtc tcc gac tgc agc gcc atc cca agg acc 299
 Leu Glu Ser Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr
 70 75 80

cag agg atg ctg aaa gca ctg tgc tct caa aag ccc gcg gca ggg att 347
 Gln Arg Met Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Ile
 85 90 95

tcc agt gaa cgc agc cga gac acc aaa att gaa gtg atc cag ttg gtg 395
 Ser Ser Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val
 100 105 110

aaa aac ctg ctg acc tat gta agg gga gtt tat cgc cat gga aat ttc 443
 Lys Asn Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe
 115 120 125

aga tgaagcatga aaacttagca tccttstctg tagaccaga cctgaccact 496
 Arg
 130

taaattccag attcattttt ctttcgcagc tcacaaattt cttaggaggagg tggggggggg 556
 ggagaacctt ttccctcagct gggacctcag cctgcacccg ctgcctccat ggagctgagc 616
 ccagccaccc ctgccttggt gcatggggcc cagccgggtg gccctcctcc gtctgcactt 676
 catcaacgct gagggaagc actgcctccc atgactgtcc cctcctcaga gcaaagtcca 736
 gcattacagt ggaggcagat atgtgtggga gggggtcttg ctgtacctgg gagtggcaca 796
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 gtgctgggga caggaggtgg cttggagctg ggggccaggt gactcgggtt tagagagtc 916
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 gccaaagcagt aatttatgtt ttttccttgt atttaagtt aagaaataaa atatgttacc 1096
 aaagagttaa taatatatag aagagttagc taaaaggctg catttggtgt gtgtggccag 1156
 gccggggcgg gtggggggga ggggtttgtc actgaatgtg ctcttccact gactttgtca 1216
 aactggaagc cagaataaaa gatgggtgaca agagaataaaa aaaaaaaa aas 1269

<210> 100

<211> 130

<212> FRT

<213> Canis familiaris

<400> 100

Met Ala Leu Trp Leu Thr Val Val Ile Ala Leu Thr Cys Leu Gly Gly
 1 5 10 15

Leu Ala Ser Pro Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu
 20 25 30

Ile Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn
 35 40 45

Gly Ser Met Val Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala
 50 55 60

Ala Leu Glu Ser Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg
 65 70 75 80

Thr Gln Arg Met Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly
 85 90 95

Ile Ser Ser Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu
 100 105 110

Val Lys Asn Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn
 115 120 125

Phe Arg
 130

<210> 101

<211> 1269

<212> DNA

<213> Canis familiaris

<400> 101

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cacacaccaa atgcagcctt ttaggtact ctctatata ttattacctt ttgataaca 180

tattttattt cttaacttta aatacaaggc aaacacataa attactgctt ggctgagggc 240

cagctgctga gtggcagacc agagcagcat ctctgacct ttctctgtc cctgtgtcg 300

gccccaggat cccagtgagg tagcagaatt ttacacacag tgcttattee cagggaacct 360

ctatccccga gtcactgggc cccagctcc aagccctcc ctgtccccag cacaaccaa 420
 gacacttgtt taantaacac acastaataa ataaggctaa gaagaaacat gtctgtgcca 480
 ctcccaggta cagcaagacc cctccccaca catatctgcc tccactgtaa tgctgcnctt 540
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 gacggaggag ggcaccccg ctggycccc tgcaccaagg cagggggtggc tgggtcagc 660
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 cccccctt aagaaattg tgacgtccga agaaaaatg aatctggaac ttaagtgtc 780
 aggtctgggt ctacagataa ggtatgtaag tttcatgct tcatctgaaa ttccatgac 840
 gataaactcc ccttaccatg gtgagcagg tttcaccaa ctggatcact tcaattttg 900
 tgtctagggt ggttccactg gaaatcccg ccgggggctt ttgagagacc agtgccttcc 960
 gcactctctg ggtcctttgg atggcgctgc agtcggagac attgatcaga gattctagag 1020
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 gactccagg gctcggggag gcaaggccac cagggcagg gtgagcaatg accacagtc 1200
 accagagacc catggagccc agagccaatg caggagagg gtgggaagag caggcaggtc 1260
 gtaggtgg 1269

<210> 102

<211> 390

<212> DNA

<213> Canis familiaris

<400> 102

atggcgctct ggttgactgt ggtcattgct ctacactgcc tccgtggcct tgcctcccc 60
 agccctgtga ctccctcccc aacctcaag gactccttg aggagctggt caccatcac 120
 caaatcagg catccctctg caacggcagc atggtgtgga ggtcaacct gaccgggc 180
 atgtactgg cagctctaga atctctgac atgtctctc actgcagcgc cctccaaag 240
 accagaggc tctgaaagc actgtgctct caaagccc cggcagggat tccagtga 300

cgcagccgag acaccsaat tgaagtgtc cagttggtga aaaacctgct cacctatgta 360
 aggggagttt atcgccatgg aaatttcaga 390

<210> 103

<211> 390

<212> DNA

<213> Canis familiaris

<400> 103

tctgaattt ccatggcgat aaactccctt tacatagggtg agcaggtttt tcaccaactg 60
 gatcaattca attttgggtgt ctccggctggc ttcactggaa atccctggcg cgggtttttg 120
 agagcacagt gotttcagca tctcttgggt ctttggatg gcgctgcagt cggagacatt 180
 gatcagagat tctagagctg cgcagtacat gccggcggtc aggttgacgc tcacacccat 240
 gctgcggttg cagagggatg cctgattctg ggtgatgttg accagctcct caatgagctc 300
 cttgagggtt ggggagggag tcacagggct cggggaggca aggccaccga ggcaggtgag 360
 agcaetgacc acagtcaccc agagcgccat 390

<210> 104

<211> 330

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> [1]..[330]

<400> 104

agc	cct	gtg	act	ccc	tcc	cxa	acc	ctc	aag	gag	ctc	att	gag	gag	ctg	48
Ser	Pro	Val	Thr	Pro	Ser	Pro	Thr	Leu	Lys	Glu	Leu	Ile	Glu	Glu	Leu	
1				5					10				15			
gtc	aac	atc	acc	cag	aat	cag	gca	tcc	ctc	tgc	aac	ggc	agc	atg	gtg	96
Val	Asn	Ile	Thr	Gln	Asn	Gln	Ala	Ser	Leu	Cys	Asn	Gly	Ser	Met	Val	
			20				25					30				
tgg	agc	gtc	aac	ctg	acc	gcc	ggc	atg	tac	tgc	gca	gct	cta	gaa	tct	144
Trp	Ser	Val	Asn	Leu	Thr	Ala	Gly	Met	Tyr	Cys	Ala	Ala	Leu	Glu	Ser	
			35				40					45				

ctg atc aat gtc tcc gac tgc agc gcc atc caa agg acc cag agg atg 192
 Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln Arg Met
 50 55 60

ctg aaa gca ctg tgc tct caa aag ccc gcg gca ggg att tcc agt gaa 240
 Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Ile Ser Ser Glu
 65 70 75 80

cgc agc cga gac acc aaa att gaa gtg atc cag ttg gtg aaa aac ctg 288
 Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val Lys Asn Leu
 85 90 95

ctc acc tat gtc agg gga gtt tat cgc cat gga aat ttc aga 330
 Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe Arg
 100 105 110

<210> 105

<211> 110

<212> PRT

<213> Canis familiaris

<400> 105

Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu Glu Leu
 1 5 10 15

Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser Met Val
 20 25 30

Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser
 35 40 45

Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln Arg Met
 50 55 60

Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Ile Ser Ser Glu
 65 70 75 80

Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val Lys Asn Leu
 85 90 95

Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe Arg
 100 105 110

<210> 106

<211> 330

<212> DNA

<213> *Canis familiaris*

<400> 106

tctgaattt ccatggcgat aaactccctt tactaggtg agcaggtttt tcaccaactg 60
gatcacttca attttgggtgt ctcggtgag ttcaactggaa atccctgccg cgggcttttg 120
agagcacagt gctttcagca tctcttgggt cctttggatg gcgctgcagt cggagacatt 180
gatcagagat tctagagctg cgcagtacat gccggcggtc aggttgacgc tccacaccat 240
gtgcgcgttg cagagggatg cctgattctg ggtgatgtg accagctctt caatgagctc 300
cttgaggggtt gggagaggag tcacagggtt 330

<210> 107

<211> 567

<212> DNA

<213> *Felis catus*

<220>

<221> CDS

<222> (1)..(567)

<400> 107

atg gcg ctg ccc tct tcc ttc ttg gtg gcc ctg gtg gcg ctg gcc tgc 48
Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
1 5 10 15
aac tcc gtc tgc tct ctg ggc tgt gac ctg cct cag acc cac gcc ctg 96
Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
20 25 30
ctg aac agg agg gcc ttg acg ctg ctg gga caa atg agg aga ctg cct 144
Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
35 40 45
gcc agc tcc tgt cag aag gac aga aat gac ttc gcc ttc ccc cag gac 192
Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp
50 55 60
gtg ttt ggt gga gac cag tcc cac aag gcc caa gcc ctg tgg gtg gtg 240
Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
65 70 75 80
cac gtg acg aac cag aag atc ttc cac ttc ttc tgc aca gag gcg tcc 288

As Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser
 85 90 95

tgg tct gct gct tgg aac acc acc ctc ctg gag gaa ttc tgc acg gga 336
 Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
 100 105 110

ctt gat tgg cag ctg acc cgc ctg gaa gcc tgt gtc atg cag gag gtg 384
 Leu Asp Trp Gln Leu Thr Arg Leu Glu Ala Cys Val Met Gln Glu Val
 115 120 125

ggg gag gga gag gct ccc ctc acg aac gag gac tcc atc ctg agg aac 432
 Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Ile Leu Arg Asn
 130 135 140

tac ttc caa aga ctc tcc ctc tac ctg caa gag aag aaa tac agc cct 480
 Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro
 145 150 155 160

tgt gcc tgg gag atc gtc aga gca gaa atc atg aga tcc ttg tat tat 528
 Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr
 165 170 175

tca tca acc gcc ttg cag aaa aga tta agg agc gag aaa 567
 Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
 180 185

<210> 108

<211> 189

<212> PRT

<213> Felis catus

<400> 108

Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
 1 5 10 15

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
 20 25 30

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
 35 40 45

Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp
 50 55 60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
 65 70 75 80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser
85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
100 105 110

Leu Asp Trp Gln Leu Thr Arg Leu Glu Ala Cys Val Met Gln Glu Val
115 120 125

Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Ile Leu Arg Asn
130 135 140

Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro
145 150 155 160

Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr
165 170 175

Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
180 185

<210> 109
<211> 567
<212> DNA
<213> Felis catus

<400> 109
cttctcgcctc cttcaatcttt tctgcaaggg tgttgatgaa taatacaagg atctcatgat 60
ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120
gagtcctttgg aagtagttcc tcaggatgga gtctcgttcc gtgaggggag cctctccctc 180
ccccacctcc tgcattgacac aggtttccag gcgggtcagc tgcattcaa gtcccgctga 240
gaattccctcc aggagggtgg tgttccaagg agcagcccgag gacgcctctg tgcagaagaa 300
gtggaagatc ttctgggttcg tcacgtgcac caccagagag gcttgggcct tgtgggactg 360
gtctccacca aacacgtcct gggggaaggg gaagtcattt ctgtccttct gacaggagct 420
ggcaggaggt ctctcattt gtcccaggag cgtccaggcc ctctgttcc gcaggccgtg 480
ggctctgaggc aggtcacagc ccagagagca gacggagttg cagcccagcg cccccagggc 540
caccaagaaq gaagaggggca ggcctat 567

<210> 110
 <211> 567
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> {1}..{567}

<400> 110
 atg gcg ctg ccc tct tcc ttc ttg gtg gcc ctg gtg gcg ctg gcc tgc 48
 Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
 1 5 10 15
 aac tcc gtc tgc tct ctg gcc tgt gac ctg cct cag acc cac gcc ctg 96
 Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
 20 25 30
 ctg aac agg agg gcc ttg acg ctc ctg gga caa atg agg aga ctc cct 144
 Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
 35 40 45
 gcc agc tcc tgt cag aag gac agg aat gac ttc gcc ttc ccc cag gac 192
 Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp
 50 55 60
 gtg ttc ggt gga gac cag tcc cac aag gct caa gcc ctc tgg gtg gtg 240
 Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
 65 70 75 80
 cac gtg acg aac cag gag stc ttc cac ttc ttc tgc aca gag gcg tcc 288
 His Val Thr Asn Gln Glu Ile Phe His Phe Phe Cys Thr Glu Ala Ser
 85 90 95
 tgg tct gct gct tgg aac acc acc ctc ctg gag gaa ttc tgc acg gga 336
 Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
 100 105 110
 ctt gat cgg cag ctg acc cgc ctg gaa gcc tgt gtc gtg cag gag gtg 384
 Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Val Gln Glu Val
 115 120 125
 ggg gag gga gag gct ccc ctc acg aac gag gac tcc ctc ctg agg aac 432
 Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Leu Leu Arg Asn
 130 135 140

tac ttc caa aga ctc tcc ctc tac ctg caa gag aag aaa tac agc cct 480
 Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro
 145 150 155 160

tgt gcc tgg gag atc gtc aga gca gaa atc atg aga tcc ttg tat tat 528
 Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr
 165 170 175

tca tca aca gcc ttg caa aaa aga tta agg agc gag aas 567
 Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
 180 185

<210> 111

<211> 189

<212> PRT

<213> Felis catus

<400> 111

Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
 1 5 10 15

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
 20 25 30

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
 35 40 45

Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp
 50 55 60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
 65 70 75 80

His Val Thr Asn Gln Glu Ile Phe His Phe Phe Cys Thr Glu Ala Ser
 85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
 100 105 110

Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Val Gln Glu Val
 115 120 125

Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Leu Leu Arg Asn
 130 135 140

Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro
 145 150 155 160

Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr
 165 170 175

Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
 180 185

<210> 112

<211> 567

<212> DNA

<213> Felis catus

<400> 112

tttctcgcgc cttcaatcttt tttgcaaggc tgttgatgaa taatacaagg atctcatgat 60
 ttctgctctg acgatctccc aggcacaaagg gctgtatttc ttctcttgca ggtagaggga 120
 gagtctttgg aagtgtttcc tcaggaggga gtctcgttc gtgaggggag cctctccctc 180
 cccacctcc tgcacgacac aggcctccag gcgggtcaga tgcagatcaa gtcccgctga 240
 gaattcctcc aggagggtgg tgttccaagg accagacgag gacgcctctg tgcagaagaa 300
 gtggaagatc tctcgggttcg tcacgtgcac caacgagagg gcttgagcct tgtgggactg 360
 gtctccaccg aacacgtcct gggggaaagg gaagtcattc ctgtccttct gacaggagct 420
 ggcagggagt ctctcatctt gtcccaggag cgtcaaggcc ctctgttcc gcaggccgtg 480
 ggtctgaggc aggtcacagc ccagagagca gacggagttg cagcccagcg ccaccagggc 540
 caccasgaag gaagagggca gcgcctat 567

<210> 113

<211> 498

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..[498]

<400> 113

tgt gac ctg cct cag acc caa ggc ctg ctg aac agg agc gcc ttg acc 48
 Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
 1 5 10 15

ctg ctg gga caa atg agg aga ctc cct gcc agc tcc tgt cag aag gac 96
 Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp
 20 25 30

aga aat gac ttc gcc ttc ccc cag gac gtg ttt ggt gga gac cag tcc 144
 Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
 35 40 45

cac aag gcc caa gcc ctc tcg gtg gtg cac gtg acg aac cag aag atc 192
 His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile
 50 55 60

ttc cac ttc ttc tgc ada gag gcg tcc tcg tat gct gct tgg aac acc 240
 Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr
 65 70 75 80

acc ctc ctg gag gaa ttc tgc acg gga ctt gat tgg cag ctg acc cgc 288
 Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Trp Gln Leu Thr Arg
 85 90 95

ctg gaa gcc tgt gtc atg cag gag gtg gga gag gga gag gct ccc ctc 336
 Leu Glu Ala Cys Val Met Gln Glu Val Gly Glu Gly Glu Ala Pro Leu
 100 105 110

acg aac gag gac tcc atc ctg agg aac tac ttc caa aga ctc tcc ctc 384
 Thr Asn Glu Asp Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu
 115 120 125

tac ctg caa gag aag aaa tac agc cct tgt gcc tgg gag atc gtc aga 432
 Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg
 130 135 140

gca gaa atc atg aga tcc ttg tat tat tca tca aca gcc ttg cag aca 480
 Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys
 145 150 155 160

aga tta agg agc gag aaa 498
 Arg Leu Arg Ser Glu Lys
 165

<210> 114

<211> 166

<212> PRT

<213> Felis catus

<400> 114

Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
 1 5 10 15

Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp
 20 25 30

Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
 35 40 45

His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile
 50 55 60

Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr
 65 70 75 80

Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Trp Gln Leu Thr Arg
 85 90 95

Leu Glu Ala Cys Val Met Gln Glu Val Gly Glu Gly Glu Ala Pro Leu
 100 105 110

Thr Asn Glu Asp Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu
 115 120 125

Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg
 130 135 140

Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys
 145 150 155 160

Arg Leu Arg Ser Glu Lys
 165

<210> 115

<211> 498

<212> DNA

<213> Felis catus

<400> 115

tttctcgttc cttactcttt tctgcaaggg tgttgatgaa caatacaagg atctcatgat 60

ttctgctctg acgactctcc aggcacaagg gctgtatttc ttctcttgca ggtcgaggga 120

gagtccttgg aagtagttcc tcaggatgga gtctcgttcc gtgagggggg cctctccctc 180

ccccacctcc tgcctgacac aggtctccag gggggtcagg tgccaatcaa gtcccggtgca 240

gaattcctcc agggagggtgg tgttcccaagc agcagacgag gacgcctctg tgcagaagaa 300
 gtggaagatc ttctggttcg tcaagtgcac caccagagagg gcttgggctt tgtgggactg 360
 gtctccacca aacacgtcct gggggaaggg gaagtcattt ctgtccttct gacaggagct 420
 ggcagggagt ctctcattt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480
 ggtctgaggg aggtcaca 498

<210> 116

<211> 498

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> {1}..{498}

<400> 116

tgt gac ctg cct cag acc cac ggc ctg ctg acc agg agg gcc ttg acg	48
Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr	
1 5 10 15	
ctc ctg gga caa atg agg aga ctc cct gcc agc tcc tgt cag aag gac	96
Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp	
20 25 30	
agg aat gac ttc gcc ttc ccc cag gac gtg ttc ggt gga gac cag tcc	144
Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser	
35 40 45	
cac aag gct caa gcc ctc tcg gtg gtg cac gtg acg aac cag gag atc	192
His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Glu Ile	
50 55 60	
ctc cac ttc ttc tgc aca gag ggg tcc tcg tct gct gct tgg aac acc	240
Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr	
65 70 75 80	
acc ctc ctg gag gaa ttc tgc acg gga ctt gat cgg cag ctg acc cgc	288
Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg	
85 90 95	
ctg gaa gcc tgt gtc gtg cag gag gtg ggg gag gga gag gct ccc ctc	336
Leu Glu Ala Cys Val Val Gln Glu Val Gly Glu Gly Glu Ala Pro Leu	
100 105 110	

acg aac gag gac tcc ctc ctg agg aac tac ttc caa aga ctc tcc ctc 384
 Thr Asn Glu Asp Ser Leu Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu
 115 120 125

tac ctg caa gag aag aac tac agc cct tgt gcc tgg gag atc gtc aga 432
 Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg
 130 135 140

gcc gaa atc atg aga tcc ttg tat tat tca tca aca gcc ttg caa aaa 480
 Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys
 145 150 155 160

aga tta agg agc gag aac 498
 Arg Leu Arg Ser Glu Lys
 165

<210> 117
 <211> 166
 <212> PRT
 <213> Pelis catus

<400> 117
 Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
 1 5 10 15

Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp
 20 25 30

Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
 35 40 45

His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Glu Ile
 50 55 60

Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr
 65 70 75 80

Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg
 85 90 95

Leu Glu Ala Cys Val Val Gln Glu Val Gly Glu Gly Glu Ala Pro Leu
 100 105 110

Thr Asn Glu Asp Ser Leu Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu
 115 120 125

Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg
 130 135 140

Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys
 145 150 155 160

Arg Leu Arg Ser Glu Lys
 165

<210> 118

<211> 498

<212> DNA

<213> Felis catus

<400> 118

ttctctgctc cttactcttt ttctgcaaggc tgttgatgaa taatacaagg atctcatgat 60
 ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120
 gagtcttttg aagtagttcc tcaggaggga gtctctgttc gtgaggggag cctctccctc 180
 cccacctcc tgcacgacac aggttccag gggggtcagc tgcgatcaa gtcccgctgc 240
 gaattctctc aggagggtgg tgtccaagc agcagacgag gacgcctctg tgcagaagaa 300
 gtggaagatc tcttggttcg tcaegtgcac caacgagagg gcttgagcct tgtgggactg 360
 gtctccaccg aacacgtcct gggggaaggc gaagtcattc ctgtccttct gacaggagct 420
 ggcaggaggt ctctcattt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480
 ggtctgaggc aggtcaca 498

<210> 119

<211> 444

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (10)..[441]

<400> 119

ggatccacc atg tgg ctg cag aac ctg ctt ttc ctg ggc aac gtg gtc tgc 51
 Met Trp Leu Gln Asn Leu Leu Phe Leu Gly Thr Val Val Cys
 1 5 10

agc atc tct gca ccc acc agt tca ccc agc tct gtc act cgg ccc atgg 99
 Ser Ile Ser Ala Pro Thr Ser Ser Pro Ser Ser Val Thr Arg Pro Trp
 15 20 25 30

 caa cac gtg gat gcc atc aag gag gcc ctg agc ctt ctg aac aac agt 147
 Gln His Val Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asn Ser
 35 40 45

 agt gaa ata act gct gtg atg aat gaa gca gta gaa gtc gtc tct gaa 195
 Ser Glu Ile Thr Ala Val Met Asn Glu Ala Val Glu Val Val Ser Glu
 50 55 60

 atg ttt gac cct gag gag ccg aaa tgc ctg cag act cac cta aag ctg 243
 Met Phe Asp Pro Glu Glu Pro Lys Cys Leu Gln Thr His Leu Lys Leu
 65 70 75

 tac gag cag ggc cta cgg ggc agc ctg atc agc ctg aag gag cct ctg 291
 Tyr Glu Gln Gly Leu Arg Gly Ser Leu Ile Ser Leu Lys Glu Pro Leu
 80 85 90

 aga atg atg gcc aac cat tac aag cag cac tgc ccc ctt act ccg gaa 339
 Arg Met Met Ala Asn His Tyr Lys Gln His Cys Pro Leu Thr Pro Glu
 95 100 105 110

 acg ccc tgt gaa acc cag act atc acc ttc aaa aat ttc aas gag aat 387
 Thr Pro Cys Glu Thr Gln Thr Ile Thr Phe Lys Asn Phe Lys Glu Asn
 115 120 125

 ctg aag gat ttt ctg ttt aac aac ccc ttt gac tgc tgg gga cca gcc 435
 Leu Lys Asp Phe Leu Phe Asn Asn Pro Phe Asp Cys Trp Gly Pro Asp
 130 135 140

 cag aag taa 444
 Gln Lys

<210> 120

<211> 144

<212> PRT

<213> Felis catus

<400> 120

Met Trp Leu Gln Asn Leu Leu Phe Leu Gly Thr Val Val Cys Ser Ile
 1 5 10 15

Ser Ala Pro Thr Ser Ser Pro Ser Ser Val Thr Arg Pro Trp Gln His
 20 25 30

Val Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asn Ser Ser Glu
35 40 45

Ile Thr Ala Val Met Asn Glu Ala Val Glu Val Val Ser Glu Met Phe
50 55 60

Asp Pro Glu Glu Pro Lys Cys Leu Gln Thr His Leu Lys Leu Tyr Glu
65 70 75 80

Gln Gly Leu Arg Gly Ser Leu Ile Ser Leu Lys Glu Pro Leu Arg Met
85 90 95

Met Ala Asn His Tyr Lys Gln His Cys Pro Leu Thr Pro Glu Thr Pro
100 105 110

Cys Glu Thr Gln Thr Ile Thr Phe Lys Asn Phe Lys Glu Asn Leu Lys
115 120 125

Asp Phe Leu Phe Asn Asn Pro Phe Asp Cys Trp Gly Pro Asp Gln Lys
130 135 140

<210> 121

<211> 444

<212> DNA

<213> Felis catus

<400> 121

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gcagtgtctg ttgtaatggt tggccatcat tctcagaggg tctttgagge tgatgaggct 180
gccccgtagg ccttgctcgt acagctttag gtgagtcctg aggcatttcg gctcctcagg 240
gtcaaacatt tcagagacga cttctactgc ttcattcacc acagcagita tttcctact 300
gttgttcaga aggtcaggg cctccttgat ggcctccacg tgttgccagg gccgagtgac 360
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<210> 122

<211> 432

<212> DNA

<213> Felis catus

<400> 122

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 agccttctga acaacagtag tgaataact gctgtgatga atgaagcagt agaagtctc 180
 tctgaaatgt ttgacctga ggagccgaaa tgcctgcaga ctacctaata gctgtacgag 240
 caggccctac ggggcagcct cctcagcctc aaggagcctc tgagaatgat ggccaacct 300
 tacaagcagc actgccccct tactccggaa acgcccctgtg aaacccagac tctcaccttc 360
 aaaaatttca aagagactct gaaggatttt ctgtttaaca accccttga ctgctgggga 420
 ccagaccaga ag 432

<210> 123

<211> 432

<212> DNA

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<400> 123

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 gggctgcttg taatggttgg ccatacttct cagaggctcc ttgaggctga tgaggctgcc 180
 ccgtaggccc tgcctgtacc gctttagggt agtctgcagg catttcggct cctcagggtc 240
 aaacatttca gagacgactt ctactgcttc attcctcaca gcagttcttt cactactgtt 300
 gttcagaagg ctccaggcct ccttgatggc atccacgtgt tgcacaggcc gactgacaga 360
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<210> 124

<211> 381

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(381)

<400> 124

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1 5 10 15	
gat gcc atc aag gag gcc ctg agc ctt ctg aac aac agt agt gaa ata	96
Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asn Ser Ser Glu Ile	
20 25 30	
act gct gtg atg aat gaa gca gta gaa gtc gtc tct gaa atg ttt gac	144
Thr Ala Val Met Asn Glu Ala Val Glu Val Val Ser Glu Met Phe Asp	
35 40 45	
cct gag gag ccg aac tgc ctg cag act cac cta aag ctg tac gag cag	192
Pro Glu Glu Pro Lys Cys Leu Gln Thr His Leu Lys Leu Tyr Glu Gln	
50 55 60	
ggc cta cgg ggc agc ctc atc agc ctc aag gag cct ctg aga atg atg	240
Gly Leu Arg Gly Ser Leu Ile Ser Leu Lys Glu Pro Leu Arg Met Met	
65 70 75 80	
gcc aac cat tac aag cag cac tgc ccc ctt act ccg gaa acg ccc tgt	288
Ala Asn His Tyr Lys Gln His Cys Pro Leu Thr Pro Glu Thr Pro Cys	
85 90 95	
gaa acc cag act atc acc ttc aaa aat ttc aac gag aat ctg aag gat	336
Glu Thr Gln Thr Ile Thr Phe Lys Asn Phe Lys Glu Asn Leu Lys Asp	
100 105 110	
ttt ctg ttt aac aac ccc ttt gac tgc tgg gga cca gac cag aag	381
Phe Leu Phe Asn Asn Pro Phe Asp Cys Trp Gly Pro Asp Gln Lys	
115 120 125	

<210> 125

<211> 127

<212> PRT

<213> Felis catus

<400> 125

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Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asn Ser Ser Glu Ile
20 25 30

Thr Ala Val Met Asn Glu Ala Val Glu Val Val Ser Glu Met Phe Asp
35 40 45

Pro Glu Glu Pro Lys Cys Leu Gln Thr His Leu Lys Leu Tyr Glu Gln
50 55 60

Gly Leu Arg Gly Ser Leu Ile Ser Leu Lys Glu Pro Leu Arg Met Met
65 70 75 80

Ala Asn His Tyr Lys Gln His Cys Pro Leu Thr Pro Glu Thr Pro Cys
85 90 95

Glu Thr Gln Thr Ile Thr Phe Lys Asn Phe Lys Glu Asn Leu Lys Asp
100 105 110

Phe Leu Phe Asn Asn Pro Phe Asp Cys Trp Gly Pro Asp Gln Lys
115 120 125

<210> 126

<211> 381

<212> DNA

<213> Felis catus

<400> 126

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gtgctgcttg tcatgggttg ccatccttct cagaggctcc ttgaggctga tgaggctgcc 180
ccgtaggccc tgctcgtaca gctttagggt agtctgcagg catttcggct cctcagggtc 240
aaacatttca gagacgactt ctactgcttc attcctcaca gcagttatct cactactgtt 300
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gctgggtgaa ctggtgggtg c 381

<210> 127

<211> 28

<212> DNA

<213> Artificial Sequence

<400> 127

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<210> 128

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

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<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 129

cgactctctt tccctctctc ctg

23

<210> 130

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

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21

<210> 131

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

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22

<210> 132

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

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28

<210> 133

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Primer

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<210> 134

<211> 16

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

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<210> 135

<211> 42

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Primer

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42

<210> 136

<211> 27

<212> DNA

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<220>

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27

<210> 137

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 137

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36

<210> 138

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 138

cccgccgccc ctaacttc cgggtgccac tc

32

<210> 139

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
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23

<210> 140

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

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23

<210> 141

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

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<400> 141

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20

<210> 142

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

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<210> 143

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

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Primer

<400> 143

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20

<210> 144

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
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<400> 144

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20

<210> 145

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

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Primer

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29

<210> 146

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 146

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<210> 147

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 147

atggcgctgc cctcttctt cttg

24

<210> 148

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

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tcatttctcg ctctttaata ttctctgc

28

<210> 149

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 149

caggatcca ccatgtgggt gcagaacctg cttttcc

37

<210> 150

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

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50

<210> 151

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
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<400> 151

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18

<210> 152

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 152

gtaatacagac tcaactatagg gc

22

<210> 153

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

Primer

<400> 153

acggaattcg agatgatagt gctggc

26

<210> 154

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 154

gtgtctagat ttgtagaaa aggatgat

28



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(51) International Patent Classification ⁶ : C12N 15/24, 15/27, 15/21, 15/12, 1/21, 5/10, C07K 14/705, 14/56, 14/54, 14/535, 14/475, 16/28, 16/24, A61K 38/19, 38/20, 38/21, 38/17, 39/395, 48/00, 39/00, 31/70, G01N 33/68	A3	(11) International Publication Number: WO 99/61618 (43) International Publication Date: 2 December 1999 (02.12.99)
(21) International Application Number: PCT/US99/11942 (22) International Filing Date: 28 May 1999 (28.05.99) (30) Priority Data: 60/087,306 29 May 1998 (29.05.98) US (71) Applicant: HESKA CORPORATION [US/US]; 1613 Prospect Parkway, Fort Collins, CO 80525 (US). (72) Inventors: SIM, Gek-Kee; 3622 Terry Point Drive, Fort Collins, CO 80524 (US). YANG, Shumin; 2624 Sha- vano Court, Fort Collins, CO 80525 (US). DREITZ, Matthew, J.; 4324 Winterstone, Fort Collins, CO 80525 (US). WONDERLING, Ramani, S.; 5808 Park Ridge Court, Fort Collins, CO 80528 (US). (74) Agents: HANLEY, Elizabeth, A. et al.; Lahive & Cockfield, LLP, 28 State Street, Boston, MA 02109 (US).		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 6 April 2000 (06.04.00)
(54) Title: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF (57) Abstract The present invention relates to canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, and/or feline GM-CSF proteins; to canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, and/or feline GM-CSF nucleic acid molecules, including those that encode canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, and/or feline GM-CSF proteins, respectively; to antibodies raised against such proteins; and to inhibitory compounds that regulate such proteins. The present invention also includes methods to identify and obtain such proteins, nucleic acid molecules, antibodies, and inhibitory compounds. Also included in the present invention are therapeutic compositions comprising such proteins, nucleic acid molecules, antibodies and/or inhibitory compounds as well as the use of such therapeutic compositions to regulate an immune response in an animal.		



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<p>(51) International Patent Classification ⁶ :</p> <p>C12N 15/24, 15/27, 15/21, 15/12, 1/21, 5/10, C07K 14/705, 14/56, 14/54, 14/535, 14/475, 16/28, 16/24, A61K 38/19, 38/20, 38/21, 38/17, 39/395, 48/00, 39/00, 31/70, G01N 33/68</p>	<p>A3</p>	<p>(11) International Publication Number: WO 99/61618</p> <p>(43) International Publication Date: 2 December 1999 (02.12.99)</p>
<p>(21) International Application Number: PCT/US99/11942</p> <p>(22) International Filing Date: 28 May 1999 (28.05.99)</p> <p>(30) Priority Data: 60/087,306 29 May 1998 (29.05.98) US</p> <p>(71) Applicant: HESKA CORPORATION [US/US]; 1613 Prospect Parkway, Fort Collins, CO 80525 (US).</p> <p>(72) Inventors: SIM, Gek-Kee; 3622 Terry Point Drive, Fort Collins, CO 80524 (US). YANG, Shumin; 2624 Shavano Court, Fort Collins, CO 80525 (US). DREITZ, Matthew, J.; 4324 Winterstone, Fort Collins, CO 80525 (US). WONDERLING, Ramani, S.; 5808 Park Ridge Court, Fort Collins, CO 80528 (US).</p> <p>(74) Agents: HANLEY, Elizabeth, A. et al.; Lahive & Cockfield, LLP, 28 State Street, Boston, MA 02109 (US).</p>		<p>(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).</p> <p>Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i></p> <p>(88) Date of publication of the international search report: 6 April 2000 (06.04.00)</p>
<p>(54) Title: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF</p> <p>(57) Abstract</p> <p>The present invention relates to canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, and/or feline GM-CSF proteins; to canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, and/or feline GM-CSF nucleic acid molecules, including those that encode canine interleukin-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154, canine interleukin-5, canine interleukin-13, feline interferon alpha, and/or feline GM-CSF proteins, respectively; to antibodies raised against such proteins; and to inhibitory compounds that regulate such proteins. The present invention also includes methods to identify and obtain such proteins, nucleic acid molecules, antibodies, and inhibitory compounds. Also included in the present invention are therapeutic compositions comprising such proteins, nucleic acid molecules, antibodies and/or inhibitory compounds as well as the use of such therapeutic compositions to regulate an immune response in an animal.</p>		

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INTERNATIONAL SEARCH REPORT

International Application No.

PCT/US 99/11942

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/24 C12N15/27 C12N15/21 C12N15/12 C12N1/21
C12N5/10 C07K14/705 C07K14/56 C07K14/54 C07K14/535
C07K14/475 C07K16/28 C07K16/24 A61K38/19 A61K38/20

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	D.L. LERNER ET AL: "Felis catus interleukin-4 mRNA" EMBL DATABASE ENTRY FCU39634, ACCESSION NUMBER U39634, 14 February 1997, XP002119488 cited in the application see abstract	3-5
A	--- EP 0 186 098 A (BOEHRINGER INGELHEIM INT) 2 July 1986 --- -/-	



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Date of the actual completion of the international search

21 October 1999

Date of mailing of the international search report

09 February 2000 (09.02.00)

Name and mailing address of the ISA

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NL - 2280 HV Rijswijk
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Fax: (+31-70) 340-3016

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INTERNATIONAL SEARCH REPORT

International Application No.

PCT/US 99/11942

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 A61K38/21 A61K38/17 A61K39/395 A61K48/00 A61K39/00
A61K31/70 G01N33/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP 0 759 468 A (VIRBAC LAB) 26 February 1997	3-5, 15, 16, 18, 20, 21, 23
A	see abstract	1, 2, 6-14, 17, 19
	see the whole document	
	see the whole document	
A	<p>--- NAOKO NAKAMURA ET AL: "Molecular cloning of feline Interferon cDNA by direct expression" BIOSCIENCE BIOTECHNOLOGY BIOCHEMISTRY., vol. 56, no. 2, 1992, JAPAN SOC. FOR BIOSCIENCE, BIOTECHNOLOGY AND AGROCHEM. TOKYO, JP, pages 211-214, XP002119489 cited in the application ---</p> <p>-/-</p>	

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *Z* document member of the same patent family

Date of the actual completion of the international search

21 October 1999

Date of mailing of the international search report

Name and mailing address of the ISA

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LE CORNEC N.D.R.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 99/11942

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	<p>S.Y. VAN DER KAAIJ ET AL: "Molecular cloning and sequencing of the cDNA for dog Interleukin-4"</p> <p>IMMUNOGENETICS,</p> <p>vol. 49, no. 2, February 1999,</p> <p>pages 142-143, XP002119490</p> <p>see the whole document</p> <p>-----</p>	<p>1-8,</p> <p>10-16,</p> <p>18-20,23</p>

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 99/ 11942

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

see FURTHER INFORMATION sheet PCT/ISA/210
2. ☒ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see additional sheet, subject 1.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box 3.

Although claims 7, 10-15, 19, 21-23, are directed to a method of treatment of the human/animal body (rule 39.1 IV PCT), the search has been carried out and based on the alleged effects of the compound/composition as far as they do not concern an inhibitor and/or a mimetope of canine interleukin-4.

Further defect(s) under Article 17(2)(a):

Continuation of Box 3.

Claims Nos.: 6b,6f,7b,7f and (21-23) partially

A meaningful search for claims 6b, 6f, 7b,7f and 21-23 partially (i.d. as far as they concern an inhibitor and/or a mimetope of an immunoregulatory protein), has not been possible because such an inhibitor and/or mimetope has not been characterized.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-23 all partially

Canine interleukin-4, nucleic acid encoding it. Method for producing said polypeptide by genetic engineering. Antibody against said polypeptide. Therapeutic composition containing canine interleukin-4, the acid nucleic encoding it or the antibody and its use in a method to regulate an immune response. Method to identify a compound capable of regulating an immune response using canine iL-4.

2. Claims: 1-23 all partially

Canine Flt-3 ligand, nucleic acid encoding it. Method for producing said polypeptide by genetic engineering. Antibody against said polypeptide. Therapeutic composition containing canine Flt-3 ligand, the acid nucleic encoding it or the antibody and its use in a method to regulate an immune response. Method to identify a compound capable of regulating an immune response using canine Flt-3 ligand.

3. Claims: 1-23 all partially

Feline Flt-3 ligand, nucleic acid encoding it. Method for producing said polypeptide by genetic engineering. Antibody against said polypeptide. Therapeutic composition containing feline Flt-3 ligand, the acid nucleic encoding it or the antibody and its use in a method to regulate an immune response. Method to identify a compound capable of regulating an immune response using feline Flt-3 ligand.

4. Claims: 1-23 all partially

Canine CD40, nucleic acid encoding it. Method for producing said polypeptide by genetic engineering. Antibody against said polypeptide. Therapeutic composition containing canine CD40, the acid nucleic encoding it or the antibody and its use in a method to regulate an immune response. Method to identify a compound capable of regulating an immune response using canine CD40.

5. Claims: 1-23 all partially

Feline CD40, nucleic acid encoding it. Method for producing said polypeptide by genetic engineering. Antibody against said polypeptide. Therapeutic composition containing feline CD40, the acid nucleic encoding it or the antibody and its use in a method to regulate an immune response. Method to identify a compound capable of regulating an immune response using feline CD40.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

6. Claims: 1-23 all partially

Canine CD154, nucleic acid encoding it. Method for producing said polypeptide by genetic engineering. Antibody against said polypeptide. Therapeutic composition containing canine CD154, the acid nucleic encoding it or the antibody and its use in a method to regulate an immune response. Method to identify a compound capable of regulating an immune response using canine CD154.

7. Claims: 1-23 all partially

Feline CD154, nucleic acid encoding it. Method for producing said polypeptide by genetic engineering. Antibody against said polypeptide. Therapeutic composition containing feline CD154, the acid nucleic encoding it or the antibody and its use in a method to regulate an immune response. Method to identify a compound capable of regulating an immune response using feline CD154.

8. Claims: 1-23 all partially

Canine interleukin-5, nucleic acid encoding it. Method for producing said polypeptide by genetic engineering. Antibody against said polypeptide. Therapeutic composition containing canine interleukin-5, the acid nucleic encoding it or the antibody and its use in a method to regulate an immune response. Method to identify a compound capable of regulating an immune response using canine interleukin-5.

9. Claims: 1-23 all partially

Canine interleukin-13, nucleic acid encoding it. Method for producing said polypeptide by genetic engineering. Antibody against said polypeptide. Therapeutic composition containing canine interleukin-13, the acid nucleic encoding it or the antibody and its use in a method to regulate an immune response. Method to identify a compound capable of regulating an immune response using canine interleukin-13.

10. Claims: 1-23 all partially

Feline interferon-alpha, nucleic acid encoding it. Method for producing said polypeptide by genetic engineering. Antibody against said polypeptide. Therapeutic composition containing feline interferon-alpha, the acid nucleic encoding it or the antibody and its use in a method to regulate an immune response. Method to identify a compound capable of regulating an immune response using feline interferon-alpha.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

11. Claims: 1-23 all partially

Feline GM-CSF, nucleic acid encoding it. Method for producing said polypeptide by genetic engineering. Antibody against said polypeptide. Therapeutic composition containing feline GM-CSF, the acid nucleic encoding it or the antibody and its use in a method to regulate an immune response. Method to identify a compound capable of regulating an immune response using feline GM-CSF.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 99/11942

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